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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Daggett, Lorrie P.  
Ellis, Steven B.  
Liaw, Chen W.  
Lu, Chin-Chun

(ii) TITLE OF INVENTION: HUMAN N-METHYL-D-ASPARTATE RECEPTOR  
SUBUNITS, NUCLEIC ACIDS ENCODING SAME AND USES THEREFOR

(iii) NUMBER OF SEQUENCES: 63

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Brown, Martin, Haller & McClain  
(B) STREET: 1660 Union Street  
(C) CITY: San Diego  
(D) STATE: CA  
(E) COUNTRY: U.S.A.  
(F) ZIP: 92101-2926

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 29-SEPT-97  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/231,193  
(B) FILING DATE: 20-APR-1994  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/052,449  
(B) FILING DATE: 20-APR-1993  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie  
(B) REGISTRATION NUMBER: 33,779  
(C) REFERENCE/DOCKET NUMBER: 6362-9383C

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-238-0999  
(B) TELEFAX: 619-238-0062

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4298 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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(A) NAME/KEY: CDS  
 (B) LOCATION: 262..3078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAAGCCGGGC GTTCGGAGCT GTGCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCTC GGCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG	240
CCAGGCCCCG GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala	291
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	339
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	387
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	435
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	579
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	627
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	675
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	723
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	771
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	819
175 180 185	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	867
190 195 200	
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	915

205	210	215	
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220	225	230	963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly 235	240	245	1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile 255	260	265	1059
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser 270	275	280	1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys 285	290	295	1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile 300	305	310	1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT .Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr 315	320	325	1251
330			
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg 335	340	345	1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val 350	355	360	1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365	370	375	1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met 380	385	390	1443
TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr 395	400	405	1491
410			
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val 415	420	425	1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr 430	435	440	1587
TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe 445	450	455	1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr 460	465	470	1683

GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	GTG	1731
Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	
475				480					485					490		
AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	ATG	GGC	GAG	CTG	CTC	1779
Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	
				495					500					505		
AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	ACC	ATA	AAC	AAC	GAG	1827
Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	
				510				515					520			
CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	AAG	TAC	CAG	GGC	CTG	1875
Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	
				525				530					535			
ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	ACG	CTG	GAC	TCG	TTC	1923
Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	
				540			545				550					
ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	GTG	GGG	CTG	TCG	GTG	1971
Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	
				555			560			565			570			
CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	CGC	TTC	AGC	CCC	TTC	2019
His	Val	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	
				575				580					585			
GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	GAC	GCA	CTG	ACC	2067	
Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr		
				590			595					600				
CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	CTG	CTC	AAC	TCC	GGC	2115
Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	
				605			610				615					
ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	CGC	ATC	CTG	GGC	ATG	2163
Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	
				620			625				630					
GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	TCC	TAC	ACC	GCC	AAC	2211
Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	Ser	Tyr	Thr	Ala	Asn	
				635			640			645			650			
CTG	GCG	GCC	TTC	CTG	GTG	GAC	CGG	CCG	GAG	GAG	CGC	ATC	ACG	GGC	2259	
Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	Glu	Arg	Ile	Thr	Gly	
				655				660					665			
ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	AAG	TTT	ATC	TAC	GCC	2307
Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	Lys	Phe	Ile	Tyr	Ala	
				670			675					680				
ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	CGG	CGC	CAG	GTG	GAG	2355
Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	Arg	Arg	Gln	Val	Glu	
				685			690				695					
CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	AAC	TAC	GAG	AGT	GCG	2403
Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	Asn	Tyr	Glu	Ser	Ala	
				700			705			710						
GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	CTG	CAT	GCC	TTC	ATC	2451
Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	Leu	His	Ala	Phe	Ile	
				715			720			725			730			
TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	CAG	AAG	TGC	GAC	CTG	2499
Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	Gln	Lys	Cys	Asp	Leu	
				735				740					745			

GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg 895 900 905	2979
GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile 910 915 920	3027
GAG AGG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser 925 930 935	3075
TGAGACTCCC CGCCCGCCCT CCTCTGCCCT CTCCCCCGCA GACAGACAGA CAGACGGACG	3135
GGACAGCGGC CCGGCCACCG CAGAGCCCCG GAGCACCAAG GGGTCGGGGG AGGAGCACCC	3195
CCAGCCTCCC CCAGGCTGCC CCTGCCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC	3255
GTCCCGGCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTCT	3315
ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCCG TCAACCTCTC AGATCCCTCG	3375
GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCCACCTG CCCAGTTAGC CGGGCCAAGG	3435
ACACTGATGG GTCTGCTGC TCGGGAAAGGC CTGAGGGAAAG CCCACCCGCC CCAGAGACTG	3495
CCCACCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCCTGGCGG GCAGCCCTG	3555
CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGCAG	3615
GGCCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG	3675

GCTAACTGCC	CCCAGGCGGA	GGGGCTTGGGA	GCAGAGACGG	CAGCCCCATC	CTTCCCGCAG	3735
CACCAGCCTG	AGCCACAGTG	GGGCCATGG	CCCCAGCTGG	CTGGGTGCGCC	CCTCCTCGGG	3795
CGCCTGGCT	CCTCTGCAGC	CTGAGCTCCA	CCCTCCCCCTC	TTCTTGCAGGC	ACCGCCCCACC	3855
AAACACCCCG	TCTGCCCTT	GACGCCACAC	GCGGGGCTG	GCGCTGCCCT	CCCCCACGGC	3915
CGTCCCTGAC	TTCCCAGCTG	GCAGCGCCTC	CCGCCGCCTC	GGGCCGCCTC	CTCCAGAACATC	3975
GAGAGGGCTG	AGCCCTCCT	CTCCTCGTCC	GGCCTGCAGC	ACAGAAGGGG	GCCTCCCCGG	4035
GGGTCCCCGG	ACGCTGGCTC	GGGACTGTCT	TCAACCCTGC	CCTGCACCTT	GGGCACGGGA	4095
GAGCGCCACC	CGCCCGCCCC	CGCCCTCGCT	CCGGGTGCGT	GACCGGCCCG	CCACCTTGTA	4155
CAGAACCAAGC	ACTCCCAGGG	CCCGAGCGCG	TGCCTTCCCC	GTGCGCAGCC	GCGCTCTGCC	4215
CCTCCGTCCC	CAGGGTGCAG	GCGGCCACCG	CCCAACCCCC	ACCTCCCGGT	GTATGCAGTG	4275
GTGATGCCTA	AAGGAATGTC	ACG				4298

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 938 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1					5			10						15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
								20			25			30	
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
								35			40			45	
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
								50		55			60		
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
								65		70		75		80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
								85		90			95		
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
								100		105			110		
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
								115		120		125			
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
								130		135		140			
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
								145		150		155		160	
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
								165		170			175		

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Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ala	Glu
180						185							190		
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu
195						200						205			
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser
210						215					220				
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met
225						230				235				240	
Thr	Gly	Ser	Gly	Tyr	Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly
									245	250			255		
Asn	Ala	Leu	Arg	Tyr	Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile
						260			265			270			
Asn	Gly	Lys	Asn	Glu	Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val
						275			280			285			
Ala	Gln	Ala	Val	His	Glu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro	
						290			295			300			
Pro	Arg	Gly	Cys	Val	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu
						305			310		315				320
Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly
						325			330			335			
Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser
						340			345			350			
Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr	Asn
						355			360			365			
Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly	Gly
						370			375			380			
Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys	Ile
						385			390		395				400
Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu	Ser
						405			410			415			
Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys
						420			425			430			
Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg
						435			440			445			
His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu	Ile
						450			455			460			
Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala
						465			470		475				480
Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys
						485			490			495			
Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met
						500			505			510			
Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu
						515			520			525			
Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys

530	535	540
Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser		
545	550	555
560		
Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met		
565	570	575
Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn		
580	585	590
Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp		
595	600	605
Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro		
610	615	620
Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala		
625	630	635
640		
Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val		
645	650	655
Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu		
660	665	670
Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser		
675	680	685
Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg		
690	695	700
His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala		
705	710	715
720		
Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu		
725	730	735
Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu		
740	745	750
Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp		
755	760	765
Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe		
770	775	780
Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser		
785	790	795
800		
Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val		
805	810	815
Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe		
820	825	830
Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met		
835	840	845
Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp		
850	855	860
Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe		
865	870	875
880		
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser		

885	890	895
Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn Gln		
900	905	910
Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln		
915	920	925
Leu Gln Leu Cys Ser Arg His Arg Glu Ser		
930	935	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 63 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC	48		
Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn			
1	5	10	15
AAG CGC GGA CCC AAG	63		
Lys Arg Gly Pro Lys			
20			

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn			
1	5	10	15
Lys Arg Gly Pro Lys			
20			

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4068 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

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## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 189..3899

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCCTTAATAA GATTTGCTAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCCGCGGGTG	60
ACGGTGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTAA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	230
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	614
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	662
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	710
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	758
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	806
195 200 205	
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	854

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	210	215	220	
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC				902
Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala	225	230	235	
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG				950
Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val	240	245	250	
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC				998
Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro	255	260	265	270
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC				1046
Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg	275	280	285	
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC				1094
Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser	290	295	300	
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT				1142
Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg	305	310	315	
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC				1190
Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His	320	325	330	
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT				1238
Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly	335	340	345	350
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC				1286
Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His	355	360	365	
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG				1334
Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met	370	375	380	
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG				1382
Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val	385	390	395	
GAC AGT CCG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC				1430
Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val	400	405	410	
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC				1478
Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr	415	420	425	430
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG				1526
Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val	435	440	445	
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC				1574
Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu	450	455	460	
AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG				1622
Lys Lys Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val	465	470	475	
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG				1670

Thr Asn Glv Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met		
480 485 490		
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC	1718	
Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu		
495 500 505 510		
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT	1766	
Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe		
515 520 525		
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC	1814	
Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val		
530 535 540		
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG	1862	
Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met		
545 550 555		
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC	1910	
Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe		
560 565 570		
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG	1958	
Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys		
575 580 585 590		
AAG TCC GGG GGC CCA GCT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG	2006	
Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu		
595 600 605		
TGG GCG CTG GTC TTC AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC	2054	
Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly		
610 615 620		
ACC ACC AGC AAG ATC ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC	2102	
Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile		
625 630 635		
TTC CTC GCC AGA TAC ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG	2150	
Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu		
640 645 650		
CAA TAC ATC GAC ACT GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG	2198	
Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg		
655 660 665 670		
CCT CAA GAT CAG TAC CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC	2246	
Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly		
675 680 685		
AGC ACG GAG CGG AAC ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC	2294	
Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His		
690 695 700		
ATG GTC AAG TTC AAC CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC	2342	
Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu		
705 710 715		
AAG ATG GGG AAG CTG GAT GCC TTC ATC TAT GAT GCT GCT GTC CTC AAC	2390	
Lys Met Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn		
720 725 730		
TAC ATG GCA GGC AAG GAC GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT	2438	
Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser		
735 740 745 750		

GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp 755	760	765	2486	
TCC CAC TGG AAG CGG GCC ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly 770	775	780	2534	
GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys 785	790	795	2582	
CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn 800	805	810	2630	
ATG GGA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG Met Gly Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu 815	820	825	830	2678
CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser 835	840	845	2726	
GTG CCC AAC TCA TCC CAG CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly 850	855	860	2774	
ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg 865	870	875	2822	
CAG GCC AGC CCG GAC CTC ACG GCC AGC TCG GCC CAG GCC AGC GTG CTC Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu 880	885	890	2870	
AAG ATT CTG CAG GCA GCC CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser 895	900	905	910	2918
AAC TCC CTG GAC CGC GCC ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly 915	920	925	2966	
CGC CGT GCG CCC CCA CCG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC Arg Arg Ala Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro 930	935	940	3014	
AGC CCA TGC CTG CCC ACC CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr 945	950	955	3062	
GGC TGG GGA CCG CCA GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala 960	965	970	3110	
CCG CAG CCC CCG GGC CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp 975	980	985	990	3158
GTC TCC CGA GTG TCG CGC CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val 995	1000	1005	3206	
CGG ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu 1010	1015	1020	3254	

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TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser 1025 1030 1035	3302
GGC CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp 1040 1045 1050	3350
CTG CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu 1055 1060 1065 1070	3398
AAC GCG GCC TGG GCC CGG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro 1075 1080 1085	3446
AGC TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly 1090 1095 1100	3494
TGC ACC GGC CCC GCC TGC GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg 1105 1110 1115	3542
CGC TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala 1120 1125 1130	3590
TGC CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln 1135 1140 1145 1150	3638
CAC GTC TGC CTG CAC GCC CAC GCA CAC CTG CCA TTG TGC TGG GGG GCT His Val Cys Leu His Ala His Leu Pro Leu Cys Trp Gly Ala 1155 1160 1165	3686
GTC TGT CCT CAC CTT CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser 1170 1175 1180	3734
GGC GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly 1185 1190 1195	3782
ACA GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala 1200 1205 1210	3830
CGT GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser 1215 1220 1225 1230	3878
AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA Ser Leu Glu Ser Glu Val 1235	3926
GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGGATTGG CCCTTCTCTG	3986
GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA	4046
TCAGTGACCT CAGCTAGCCT CA	4068

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1236 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly  
1                   5                   10                   15

Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val  
20               25               30

Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val  
35               40               45

Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro  
50               55               60

Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln  
65               70               75               80

Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu  
85               90               95

Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser  
100              105              110

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val  
115              120              125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val  
130              135              140

Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr  
145              150              155              160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala  
165              170              175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser  
180              185              190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro  
195              200              205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe  
210              215              220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala  
225              230              235              240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn  
245              250              255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly  
260              265              270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys  
275              280              285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp  
290              295              300

Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His  
305              310              315              320

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Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu  
 325 330 335  
 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr  
 340 345 350  
 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu  
 355 360 365  
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr  
 370 375 380  
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser  
 385 390 395 400  
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val  
 405 410 415  
 Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro  
 420 425 430  
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro  
 435 440 445  
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys  
 450 455 460  
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn  
 465 470 475 480  
 Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly  
 485 490 495  
 Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile  
 500 505 510  
 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu  
 515 520 525  
 Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro  
 530 535 540  
 Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe  
 545 550 555 560  
 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr  
 565 570 575  
 Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser  
 580 585 590  
 Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala  
 595 600 605  
 Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr  
 610 615 620  
 Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu  
 625 630 635 640  
 Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr  
 645 650 655  
 Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln  
 660 665 670

Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr  
675 680 685

Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val  
690 695 700

Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met  
705 710 715 720

Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met  
725 730 735

Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys  
740 745 750

Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His  
755 760 765

Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly  
770 775 780

Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn  
785 790 795 800

Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly  
805 810 815

Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Val  
820 825 830

Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro  
835 840 845

Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr  
850 855 860

Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala  
865 870 875 880

Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile  
885 890 895

Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser  
900 905 910

Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg  
915 920 925

Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro  
930 935 940

Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp  
945 950 955 960

Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln  
965 970 975

Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser  
980 985 990

Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr  
995 1000 1005

Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro  
1010 1015 1020

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Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg  
1025 1030 1035 1040

Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro  
1045 1050 1055

Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala  
1060 1065 1070

Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser  
1075 1080 1085

Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr  
1090 1095 1100

Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu  
1105 1110 1115 1120

Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln  
1125 1130 1135

Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val  
1140 1145 1150

Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys  
1155 1160 1165

Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala  
1170 1175 1180

Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly  
1185 1190 1195 1200

Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly  
1205 1210 1215

Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu  
1220 1225 1230

Glu Ser Glu Val  
1235

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 2..22

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

C TCT GAG GCT CAG CCT GTC CCC AG  
Ser Glu Ala Gln Pro Val Pro  
1 5

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## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Glu Ala Gln Pro Val Pro  
1 5

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGAAGGGGGT G 11

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4808 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 311..4705

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATCATGGGAC CGGGTGAGCG CTGAGAACATCG CGGCCGCAGC CATCAGCCCT GGAGATGACC	60
AGGAGCGGCC ACTGCTGAGA ACTATGTGGA GAGAGGCTGC GAGCCCTGCT GCAGAGCCTC	120
CGGCTGGGAT AGCCGCCCG CGTGGGGCG ATGCGGACAG CGCGGGACAG CCAGGGGAGC	180
GCGCTGGGC CGCAGCATGC GGGAAACCGC TAAACCCGGT GGCTGCTGAG GCGGCCGAGA	240
TGCTCGTGCG CGCAGCGCGC CCCACTGCAT CCTCGACCTT CTCGGGCTAC AGGGACCGTC	300
AGTGGCGACT ATG GGC AGA GTG GGC TAT TGG ACC CTG CTG GTG CTG CCG Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro	349
1 5 10	
GCC CTT CTG GTC TGG CGC GGT CCG GCG CCG AGC GCG GCG GCG GAG AAG Ala Leu Leu Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys	397
15 20 25	
GGT CCC CCC GCG CTA AAT ATT GCG GTG ATG CTG GGT CAC AGC CAC GAC	445

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Gly Pro Pro Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp				
30 35 40 45				
GTG ACA GAG CGC GAA CTT CGA ACA CTG TGG GGC CCC GAG CAG GCG GCG				493
Val Thr Glu Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala				
50 55 60				
GGG CTG CCC CTG GAC GTG AAC GTG GTA GCT CTG ATG AAC CGC ACC				541
Gly Leu Pro Leu Asp Val Asn Val Ala Leu Leu Met Asn Arg Thr				
65 70 75				
GAC CCC AAG AGC CTC ATC ACG CAC GTG TGC GAC CTC ATG TCC GGG GCA				589
Asp Pro Lys Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala				
80 85 90				
CGC ATC CAC GGC CTC GTG TTT GGG GAC GAC ACG GAC CAG GAG GCC GTA				637
Arg Ile His Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val				
95 100 105				
GCC CAG ATG CTG GAT TTT ATC TCC TCC CAC ACC TTC GTC CCC ATC TTG				685
Ala Gln Met Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu				
110 115 120 125				
GGC ATT CAT GGG GGC GCA TCT ATG ATC ATG GCT GAC AAG GAT CCG ACG				733
Gly Ile His Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr				
130 135 140				
TCT ACC TTC TTC CAG TTT GGA GCG TCC ATC CAG CAG CAA GCC ACG GTC				781
Ser Thr Phe Gln Phe Gly Ala Ser Ile Gln Gln Gln Ala Thr Val				
145 150 155				
ATG CTG AAG ATC ATG CAG GAT TAT GAC TGG CAT GTC TTC TCC CTG GTG				829
Met Leu Lys Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val				
160 165 170				
ACC ACT ATC TTC CCT GGC TAC AGG GAA TTC ATC AGC TTC GTC AAG ACC				877
Thr Thr Ile Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr				
175 180 185				
ACA GTG GAC AAC AGC TTT GTG GGC TGG GAC ATG CAG AAT GTG ATC ACA				925
Thr Val Asp Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr				
190 195 200 205				
CTG GAC ACT TCC TTT GAG GAT GCA AAG ACA CAA GTC CAG CTG AAG AAG				973
Leu Asp Thr Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys				
210 215 220				
ATC CAC TCT TCT GTC ATC TTG CTC TAC TGT TCC AAA GAC GAG GCT GTT				1021
Ile His Ser Ser Val Ile Leu Tyr Cys Ser Lys Asp Glu Ala Val				
225 230 235				
CTC ATT CTG AGT GAG GCC CGC TCC CTT GGC CTC ACC GGG TAT GAT TTC				1069
Leu Ile Leu Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe				
240 245 250				
TTC TGG ATT GTC CCC AGC TTG GTC TCT GGG AAC ACG GAG CTC ATC CCA				1117
Phe Trp Ile Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro				
255 260 265				
AAA GAG TTT CCA TCG GGA CTC ATT TCT GTC TCC TAC GAT GAC TGG GAC				1165
Lys Glu Phe Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp				
270 275 280 285				
TAC AGC CTG GAG GCG AGA GTG AGG GAC GGC ATT GGC ATC CTA ACC ACC				1213
Tyr Ser Leu Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr				
290 295 300				

GCT GCA TCT TCT ATG CTG GAG AAG TTC TCC TAC ATC CCC GAG GCC AAG Ala Ala Ser Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys 305 310 315	1261
GCC AGC TGC TAC GGG CAG ATG GAG AGG CCA GAG GTC CCG ATG CAC ACC Ala Ser Cys Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr 320 325 330	1309
TTG CAC CCA TTT ATG GTC AAT GTT ACA TGG GAT GGC AAA GAC TTA TCC Leu His Pro Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser 335 340 345	1357
TTC ACT GAG GAA GGC TAC CAG GTG CAC CCC AGG CTG GTG GTG ATT GTG Phe Thr Glu Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val 350 355 360 365	1405
CTG AAC AAA GAC CGG GAA TGG GAA AAG GTG GGC AAG TGG GAG AAC CAT Leu Asn Lys Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His 370 375 380	1453
ACG CTG AGC CTG AGG CAC GCC GTG TGG CCC AGG TAC AAG TCC TTC TCC Thr Leu Ser Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser 385 390 395	1501
GAC TGT GAG CCG GAT GAC AAC CAT CTC AGC ATC GTC ACC CTG GAG GAG Asp Cys Glu Pro Asp Asn His Leu Ser Ile Val Thr Leu Glu Glu 400 405 410	1549
GCC CCA TTC GTC ATC GTG GAA GAC ATA GAC CCC CTG ACC GAG ACG TGT Ala Pro Phe Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys 415 420 425	1597
G TG AGG AAC ACC GTG CCA TGT CGG AAG TTC GTC AAA ATC AAC AAT TCA Val Arg Asn Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser 430 435 440 445	1645
ACC AAT GAG GGG ATG AAT GTG AAG AAA TGC TGC AAG GGG TTC TGC ATT Thr Asn Glu Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile 450 455 460	1693
GAT ATT CTG AAG AAG CTT TCC AGA ACT GTG AAG TTT ACT TAC GAC CTC Asp Ile Leu Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu 465 470 475	1741
TAT CTG GTG ACC AAT GGG AAG CAT GGC AAG AAA GTT AAC AAT GTG TGG Tyr Leu Val Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp 480 485 490	1789
AAT GGA ATG ATC GGT GAA GTG GTC TAT CAA CGG GCA GTC ATG GCA GTT Asn Gly Met Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val 495 500 505	1837
GGC TCG CTC ACC ATC AAT GAG GAA CGT TCT GAA GTG GTG GAC TTC TCT Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser 510 515 520 525	1885
G TG CCC TTT GTG GAA ACG GGA ATC AGT GTC ATG GTT TCA AGA AGT AAT Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn 530 535 540	1933
GGC ACC GTC TCA CCT TCT GCT TTT CTA GAA CCA TTC AGC GCC TCT GTC Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val 545 550 555	1981
TGG GTG ATG ATG TTT GTG ATG CTG CTC ATT GTT TCT GCC ATA GCT GTT Trp Val Met Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val 560 565 570	2029

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TGG GTC TTG GAT TAC TCC AGC CCT GTT GGA TAC AAC AGA AAC TTA GCC Trp Val Leu Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala 575 580 585	2077
AAA GGG AAA GCA CCC CAT GGG CCT TCT TTT ACA ATT GGA AAA GCT ATA Lys Gly Lys Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile 590 595 600 605	2125
TGG CTT CTT TGG GGC CTG GTG TTC AAT AAC TCC GTG CCT GTC CAG AAT Trp Leu Leu Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn 610 615 620	2173
CCT AAA GGG ACC ACC AGC AAG ATC ATG GTA TCT GTA TGG GCC TTC TTC Pro Lys Gly Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe 625 630 635	2221
GCT GTC ATA TTC CTG GCT AGC TAC ACA GCC AAT CTG GCT GCC TTC ATG Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met 640 645 650	2269
ATC CAA GAG GAA TTT GTG GAC CAA GTG ACC GGC CTC AGT GAC AAA AAG Ile Gln Glu Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys 655 660 665	2317
TTT CAG AGA CCT CAT GAC TAT TCC CCA CCT TTT CGA TTT GGG ACA GTG Phe Gln Arg Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val 670 675 680 685	2365
CCT AAT GGA AGC ACG GAG AGA AAC ATT CGG AAT AAC TAT CCC TAC ATG Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met 690 695 700	2413
CAT CAG TAC ATG ACC AAA TTT AAT CAG AAA GGA GTA GAG GAC GCC TTG His Gln Tyr Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu 705 710 715	2461
GTC AGC CTG AAA ACG GGG AAG CTG GAC GCT TTC ATC TAC GAT GCC GCA Val Ser Leu Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala 720 725 730	2509
GTC TTG AAT TAC AAG GCT GGG AGG GAT GAA GGC TGC AAG CTG GTG ACC Val Leu Asn Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr 735 740 745	2557
ATC GGG AGT GGG TAC ATC TTT GCC ACC ACC GGT TAT GGA ATT GCC CTT Ile Gly Ser Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu 750 755 760 765	2605
CAG AAA GGC TCT CCT TGG AAG AGG CAG ATC GAC CTG GCC TTG CTT CAG Gln Lys Gly Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Leu Gln 770 775 780	2653
TTT GTG GGT GAT GGT GAG ATG GAG GAG CTG GAG ACC CTG TGG CTC ACT Phe Val Gly Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr 785 790 795	2701
GGG ATC TGC CAC AAC GAG AAG AAC GAG GTG ATG AGC AGC CAG CTG GAC Gly Ile Cys His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp 800 805 810	2749
ATT GAC AAC ATG GCG GGC GTA TTC TAC ATG CTG GCT GCC GCC ATG GCC Ile Asp Asn Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala 815 820 825	2797
CTT AGC CTC ATC ACC TTC ATC TGG GAG CAC CTC TTC TAC TGG AAG CTG Leu Ser Leu Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu 830 835 840 845	2845

CGC TTC TGT TTC ACG GGC GTG TGC TCC GAC CGG CCT GGG TTG CTC TTC Arg Phe Cys Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe 850 855 860	2893
TCC ATC AGC AGG GGC ATC TAC AGC TGC ATT CAT GGA GTG CAC ATT GAA Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu 865 870 875	2941
GAA AAG AAG AAG TCT CCA GAC TTC AAT CTG ACG GGA TCC CAG AGC AAC Glu Lys Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn 880 885 890	2989
ATG TTA AAA CTC CTC CGG TCA GCC AAA AAC ATT TCC AGC ATG TCC AAC Met Leu Lys Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn 895 900 905	3037
ATG AAC TCC TCA AGA ATG GAC TCA CCC AAA AGA GCT GCT GAC TTC ATC Met Asn Ser Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile 910 915 920 925	3085
CAA AGA GGT TCC CTC ATC ATG GAC ATG GTT TCA GAT AAG GGG AAT TTG Gln Arg Gly Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu 930 935 940	3133
ATG TAC TCA GAC AAC AGG TCC TTT CAG GGG AAA GAG AGC ATT TTT GGA Met Tyr Ser Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly 945 950 955	3181
GAC AAC ATG AAC GAA CTC CAA ACA TTT GTG GCC AAC CGG CAG AAG GAT Asp Asn Met Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp 960 965 970	3229
AAC CTC AAT AAC TAT GTA TTC CAG GGA CAA CAT CCT CTT ACT CTC AAT Asn Leu Asn Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn 975 980 985	3277
GAG TCC AAC CCT AAC ACG GTG GAG GTG GCC GTG AGC ACA GAA TCC AAA Glu Ser Asn Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys 990 995 1000 1005	3325
GCG AAC TCT AGA CCC CGG CAG CTG TGG AAG AAA TCC GTG GAT TCC ATA Ala Asn Ser Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile 1010 1015 1020	3373
CGC CAG GAT TCA CTA TCC CAG AAT CCA GTC TCC CAG AGG GAT GAG GCA Arg Gln Asp Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala 1025 1030 1035	3421
ACA GCA GAG AAT AGG ACC CAC TCC CTA AAG AGC CCT AGG TAT CTT CCA Thr Ala Glu Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro 1040 1045 1050	3469
GAA GAG ATG GCC CAC TCT GAC ATT TCA GAA ACG TCA AAT CGG GCC ACG Glu Glu Met Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr 1055 1060 1065	3517
TGC CAC AGG GAA CCT GAC AAC AGT AAG AAC CAC AAA ACC AAG GAC AAC Cys His Arg Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn 1070 1075 1080 1085	3565
TTT AAA AGG TCA GTG GCC TCC AAA TAC CCC AAG GAC TGT AGT GAG GTC Phe Lys Arg Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val 1090 1095 1100	3613
GAG CGC ACC TAC CTG AAA ACC AAA TCA AGC TCC CCT AGA GAC AAG ATC Glu Arg Thr Tyr Leu Lys Thr Lys Ser Ser Ser Pro Arg Asp Lys Ile 1105 1110 1115	3661

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TAC ACT ATA GAT GGT GAG AAG GAG CCT GGT TTC CAC TTA GAT CCA CCC Tyr Thr Ile Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro 1120 1125 1130	3709
CAG TTT GTT GAA AAT GTG ACC CTG CCC GAG AAC GTG GAC TTC CCG GAC Gln Phe Val Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp 1135 1140 1145	3757
CCC TAC CAG GAT CCC AGT GAA AAC TTC CGC AAG GGG GAC TCC ACG CTG Pro Tyr Gln Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu 1150 1155 1160 1165	3805
CCA ATG AAC CGG AAC CCC TTG CAT AAT GAA GAG GGG CTT TCC AAC AAC Pro Met Asn Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn 1170 1175 1180	3853
GAC CAG TAT AAA CTC TAC TCC AAG CAC TTC ACC TTG AAA GAC AAG GGT Asp Gln Tyr Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly 1185 1190 1195	3901
TCC CCG CAC AGT GAG ACC AGC GAG CGA TAC CGG CAG AAC TCC ACG CAC Ser Pro His Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His 1200 1205 1210	3949
TGC AGA AGC TGC CTT TCC AAC ATG CCC ACC TAT TCA GGC CAC TTC ACC Cys Arg Ser Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr 1215 1220 1225	3997
ATG AGG TCC CCC TTC AAG TGC GAT GCC TGC CTG CGG ATG GGG AAC CTC Met Arg Ser Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu 1230 1235 1240 1245	4045
TAT GAC ATC GAT GAA GAC CAG ATG CTT CAG GAG ACA GGT AAC CCA GCC Tyr Asp Ile Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala 1250 1255 1260	4093
ACC GGG GAG CAG GTC TAC CAG CAG GAC TGG GCA CAG AAC AAT GCC CTT Thr Gly Gln Val Tyr Gln Asp Trp Ala Gln Asn Asn Ala Leu 1265 1270 1275	4141
CAA TTA CAA AAG AAC AAG CTA AGG ATT AGC CGT CAG CAT TCC TAC GAT Gln Leu Gln Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp 1280 1285 1290	4189
AAC ATT GTC GAC AAA CCT AGG GAG CTA GAC CTT AGC AGG CCC TCC CGG Asn Ile Val Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg 1295 1300 1305	4237
AGC ATA AGC CTC AAG GAC AGG GAA CGG CTT CTG GAG GGA AAT TTT TAC Ser Ile Ser Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr 1310 1315 1320 1325	4285
GGC AGC CTG TTT AGT GTC CCC TCA AGC AAA CTC TCG GGG AAA AAA AGC Gly Ser Leu Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser 1330 1335 1340	4333
TCC CTT TTC CCC CAA GGT CTG GAG GAC AGC AAG AGG AGC AAG TCT CTC Ser Leu Phe Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu 1345 1350 1355	4381
TTG CCA GAC CAC ACC TCC GAT AAC CCT TTC CTC CAC TCC CAC AGG GAT Leu Pro Asp His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp 1360 1365 1370	4429
GAC CAA CGC TTG GTT ATT GGG AGA TGC CCC TCG GAC CCT TAC AAA CAC Asp Gln Arg Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His 1375 1380 1385	4477

TCG TTG CCA TCC CAG GCG GTG AAT GAC AGC TAT CTT CGG TCG TCC TTG Ser Leu Pro Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu 1390 1395 1400 1405	4525
AGG TCA ACG GCA TCG TAC TGT TCC AGG GAC AGT CGG GGC CAC AAT GAT Arg Ser Thr Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp 1410 1415 1420	4573
G TG TAT ATT TCG GAG CAT GTT ATG CCT TAT GCT GCA AAT AAG AAT AAT Val Tyr Ile Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn 1425 1430 1435	4621
ATG TAC TCT ACC CCC AGG GTT TTA AAT TCC TGC AGC AAT AGA CGC GTG Met Tyr Ser Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val 1440 1445 1450	4669
TAC AAG GAA ATG CCT AGT ATC GAA TCT GAT GTT TAAAAATCTT CCATTAATGT Tyr Lys Glu Met Pro Ser Ile Glu Ser Asp Val 1455 1460 146	4722
TTTATCTATA GGGAAATACA CGTAATGCC AATGTTCTGG AGGGTAAATG TTGGATGTCC AATAGTGCCC TGCTAACAGGG AAGGAG	4782
	4808

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1464 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Arg Val Gly Tyr Trp Thr Leu Leu Val Leu Pro Ala Leu Leu 1 5 10 15
Val Trp Arg Gly Pro Ala Pro Ser Ala Ala Ala Glu Lys Gly Pro Pro 20 25 30
Ala Leu Asn Ile Ala Val Met Leu Gly His Ser His Asp Val Thr Glu 35 40 45
Arg Glu Leu Arg Thr Leu Trp Gly Pro Glu Gln Ala Ala Gly Leu Pro 50 55 60
Leu Asp Val Asn Val Val Ala Leu Leu Met Asn Arg Thr Asp Pro Lys 65 70 75 80
Ser Leu Ile Thr His Val Cys Asp Leu Met Ser Gly Ala Arg Ile His 85 90 95
Gly Leu Val Phe Gly Asp Asp Thr Asp Gln Glu Ala Val Ala Gln Met 100 105 110
Leu Asp Phe Ile Ser Ser His Thr Phe Val Pro Ile Leu Gly Ile His 115 120 125
Gly Gly Ala Ser Met Ile Met Ala Asp Lys Asp Pro Thr Ser Thr Phe 130 135 140
Phe Gln Phe Gly Ala Ser Ile Gln Gln Ala Thr Val Met Leu Lys 145 150 155 160
Ile Met Gln Asp Tyr Asp Trp His Val Phe Ser Leu Val Thr Thr Ile

	165	170	175
Phe Pro Gly Tyr Arg Glu Phe Ile Ser Phe Val Lys Thr Thr Val Asp			
180	185		190
Asn Ser Phe Val Gly Trp Asp Met Gln Asn Val Ile Thr Leu Asp Thr			
195	200		205
Ser Phe Glu Asp Ala Lys Thr Gln Val Gln Leu Lys Lys Ile His Ser			
210	215		220
Ser Val Ile Leu Leu Tyr Cys Ser Lys Asp Glu Ala Val Leu Ile Leu			
225	230	235	240
Ser Glu Ala Arg Ser Leu Gly Leu Thr Gly Tyr Asp Phe Phe Trp Ile			
245	250	250	255
Val Pro Ser Leu Val Ser Gly Asn Thr Glu Leu Ile Pro Lys Glu Phe			
260	265		270
Pro Ser Gly Leu Ile Ser Val Ser Tyr Asp Asp Trp Asp Tyr Ser Leu			
275	280		285
Glu Ala Arg Val Arg Asp Gly Ile Gly Ile Leu Thr Thr Ala Ala Ser			
290	295		300
Ser Met Leu Glu Lys Phe Ser Tyr Ile Pro Glu Ala Lys Ala Ser Cys			
305	310	315	320
Tyr Gly Gln Met Glu Arg Pro Glu Val Pro Met His Thr Leu His Pro			
325	330	330	335
Phe Met Val Asn Val Thr Trp Asp Gly Lys Asp Leu Ser Phe Thr Glu			
340	345		350
Glu Gly Tyr Gln Val His Pro Arg Leu Val Val Ile Val Leu Asn Lys			
355	360		365
Asp Arg Glu Trp Glu Lys Val Gly Lys Trp Glu Asn His Thr Leu Ser			
370	375		380
Leu Arg His Ala Val Trp Pro Arg Tyr Lys Ser Phe Ser Asp Cys Glu			
385	390	395	400
Pro Asp Asp Asn His Leu Ser Ile Val Thr Leu Glu Ala Pro Phe			
405	410		415
Val Ile Val Glu Asp Ile Asp Pro Leu Thr Glu Thr Cys Val Arg Asn			
420	425		430
Thr Val Pro Cys Arg Lys Phe Val Lys Ile Asn Asn Ser Thr Asn Glu			
435	440		445
Gly Met Asn Val Lys Lys Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu			
450	455	460	
Lys Lys Leu Ser Arg Thr Val Lys Phe Thr Tyr Asp Leu Tyr Leu Val			
465	470	475	480
Thr Asn Gly Lys His Gly Lys Lys Val Asn Asn Val Trp Asn Gly Met			
485	490		495
Ile Gly Glu Val Val Tyr Gln Arg Ala Val Met Ala Val Gly Ser Leu			
500	505		510
Thr Ile Asn Glu Glu Arg Ser Glu Val Val Asp Phe Ser Val Pro Phe			
515	520		525

Val Glu Thr Gly Ile Ser Val Met Val Ser Arg Ser Asn Gly Thr Val  
530 535 540

Ser Pro Ser Ala Phe Leu Glu Pro Phe Ser Ala Ser Val Trp Val Met  
545 550 555 560

Met Phe Val Met Leu Leu Ile Val Ser Ala Ile Ala Val Trp Val Leu  
565 570 575

Asp Tyr Ser Ser Pro Val Gly Tyr Asn Arg Asn Leu Ala Lys Gly Lys  
580 585 590

Ala Pro His Gly Pro Ser Phe Thr Ile Gly Lys Ala Ile Trp Leu Leu  
595 600 605

Trp Gly Leu Val Phe Asn Asn Ser Val Pro Val Gln Asn Pro Lys Gly  
610 615 620

Thr Thr Ser Lys Ile Met Val Ser Val Trp Ala Phe Phe Ala Val Ile  
625 630 635 640

Phe Leu Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu  
645 650 655

Glu Phe Val Asp Gln Val Thr Gly Leu Ser Asp Lys Lys Phe Gln Arg  
660 665 670

Pro His Asp Tyr Ser Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly  
675 680 685

Ser Thr Glu Arg Asn Ile Arg Asn Asn Tyr Pro Tyr Met His Gln Tyr  
690 695 700

Met Thr Lys Phe Asn Gln Lys Gly Val Glu Asp Ala Leu Val Ser Leu  
705 710 715 720

Lys Thr Gly Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn  
725 730 735

Tyr Lys Ala Gly Arg Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser  
740 745 750

Gly Tyr Ile Phe Ala Thr Thr Gly Tyr Gly Ile Ala Leu Gln Lys Gly  
755 760 765

Ser Pro Trp Lys Arg Gln Ile Asp Leu Ala Leu Gln Phe Val Gly  
770 775 780

Asp Gly Glu Met Glu Glu Leu Glu Thr Leu Trp Leu Thr Gly Ile Cys  
785 790 795 800

His Asn Glu Lys Asn Glu Val Met Ser Ser Gln Leu Asp Ile Asp Asn  
805 810 815

Met Ala Gly Val Phe Tyr Met Leu Ala Ala Ala Met Ala Leu Ser Leu  
820 825 830

Ile Thr Phe Ile Trp Glu His Leu Phe Tyr Trp Lys Leu Arg Phe Cys  
835 840 845

Phe Thr Gly Val Cys Ser Asp Arg Pro Gly Leu Leu Phe Ser Ile Ser  
850 855 860

Arg Gly Ile Tyr Ser Cys Ile His Gly Val His Ile Glu Glu Lys Lys  
865 870 875 880

Lys Ser Pro Asp Phe Asn Leu Thr Gly Ser Gln Ser Asn Met Leu Lys

885	890	895
Leu Leu Arg Ser Ala Lys Asn Ile Ser Ser Met Ser Asn Met Asn Ser		
900	905	910
Ser Arg Met Asp Ser Pro Lys Arg Ala Ala Asp Phe Ile Gln Arg Gly		
915	920	925
Ser Leu Ile Met Asp Met Val Ser Asp Lys Gly Asn Leu Met Tyr Ser		
930	935	940
Asp Asn Arg Ser Phe Gln Gly Lys Glu Ser Ile Phe Gly Asp Asn Met		
945	950	955
960		
Asn Glu Leu Gln Thr Phe Val Ala Asn Arg Gln Lys Asp Asn Leu Asn		
965	970	975
Asn Tyr Val Phe Gln Gly Gln His Pro Leu Thr Leu Asn Glu Ser Asn		
980	985	990
Pro Asn Thr Val Glu Val Ala Val Ser Thr Glu Ser Lys Ala Asn Ser		
995	1000	1005
Arg Pro Arg Gln Leu Trp Lys Lys Ser Val Asp Ser Ile Arg Gln Asp		
1010	1015	1020
Ser Leu Ser Gln Asn Pro Val Ser Gln Arg Asp Glu Ala Thr Ala Glu		
1025	1030	1035
1040		
Asn Arg Thr His Ser Leu Lys Ser Pro Arg Tyr Leu Pro Glu Glu Met		
1045	1050	1055
Ala His Ser Asp Ile Ser Glu Thr Ser Asn Arg Ala Thr Cys His Arg		
1060	1065	1070
Glu Pro Asp Asn Ser Lys Asn His Lys Thr Lys Asp Asn Phe Lys Arg		
1075	1080	1085
Ser Val Ala Ser Lys Tyr Pro Lys Asp Cys Ser Glu Val Glu Arg Thr		
1090	1095	1100
Tyr Leu Lys Thr Lys Ser Ser Pro Arg Asp Lys Ile Tyr Thr Ile		
1105	1110	1115
1120		
Asp Gly Glu Lys Glu Pro Gly Phe His Leu Asp Pro Pro Gln Phe Val		
1125	1130	1135
Glu Asn Val Thr Leu Pro Glu Asn Val Asp Phe Pro Asp Pro Tyr Gln		
1140	1145	1150
Asp Pro Ser Glu Asn Phe Arg Lys Gly Asp Ser Thr Leu Pro Met Asn		
1155	1160	1165
Arg Asn Pro Leu His Asn Glu Glu Gly Leu Ser Asn Asn Asp Gln Tyr		
1170	1175	1180
Lys Leu Tyr Ser Lys His Phe Thr Leu Lys Asp Lys Gly Ser Pro His		
1185	1190	1195
1200		
Ser Glu Thr Ser Glu Arg Tyr Arg Gln Asn Ser Thr His Cys Arg Ser		
1205	1210	1215
Cys Leu Ser Asn Met Pro Thr Tyr Ser Gly His Phe Thr Met Arg Ser		
1220	1225	1230
Pro Phe Lys Cys Asp Ala Cys Leu Arg Met Gly Asn Leu Tyr Asp Ile		
1235	1240	1245

Asp Glu Asp Gln Met Leu Gln Glu Thr Gly Asn Pro Ala Thr Gly Glu  
1250 1255 1260

Gln Val Tyr Gln Gln Asp Trp Ala Gln Asn Asn Ala Leu Gln Leu Gln  
1265 1270 1275 1280

Lys Asn Lys Leu Arg Ile Ser Arg Gln His Ser Tyr Asp Asn Ile Val  
1285 1290 1295

Asp Lys Pro Arg Glu Leu Asp Leu Ser Arg Pro Ser Arg Ser Ile Ser  
1300 1305 1310

Leu Lys Asp Arg Glu Arg Leu Leu Glu Gly Asn Phe Tyr Gly Ser Leu  
1315 1320 1325

Phe Ser Val Pro Ser Ser Lys Leu Ser Gly Lys Lys Ser Ser Leu Phe  
1330 1335 1340

Pro Gln Gly Leu Glu Asp Ser Lys Arg Ser Lys Ser Leu Leu Pro Asp  
1345 1350 1355 1360

His Thr Ser Asp Asn Pro Phe Leu His Ser His Arg Asp Asp Gln Arg  
1365 1370 1375

Leu Val Ile Gly Arg Cys Pro Ser Asp Pro Tyr Lys His Ser Leu Pro  
1380 1385 1390

Ser Gln Ala Val Asn Asp Ser Tyr Leu Arg Ser Ser Leu Arg Ser Thr  
1395 1400 1405

Ala Ser Tyr Cys Ser Arg Asp Ser Arg Gly His Asn Asp Val Tyr Ile  
1410 1415 1420

Ser Glu His Val Met Pro Tyr Ala Ala Asn Lys Asn Asn Met Tyr Ser  
1425 1430 1435 1440

Thr Pro Arg Val Leu Asn Ser Cys Ser Asn Arg Arg Val Tyr Lys Glu  
1445 1450 1455

Met Pro Ser Ile Glu Ser Asp Val  
1460

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 74 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGAGGGAGGC GGCCGGCGCG GACTCTCTTC GCAGGGCGCAG CGCCCCTTCC CCCTCGGACC 60  
CTCCGGTGGGA CATG 74

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3155 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 262..3030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	

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	175	180	185	
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 190	195		200	867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val 205		210	215	915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220	225		230	963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly 235	240		245	1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile 255		260	265	1059
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser 270	275		280	1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys 285		290	295	1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile 300	305		310	1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr 315	320		325	1251
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg 335		340	345	1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val 350	355		360	1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys 365		370	375	1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met 380	385		390	1443
TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr 395	400		405	1491
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val 415		420	425	1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr 430	435		440	1587

TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe 445 450 455	1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr 460 465 470	1683
GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val 475 480 485 490	1731
AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu 495 500 505	1779
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu 510 515 520	1827
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu 525 530 535	1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe 540 545 550	1923
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val 555 560 565 570	1971
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe 575 580 585	2019
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr 590 595 600	2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly 605 610 615	2115
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met 620 625 630	2163
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn 635 640 645 650	2211
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly 655 660 665	2259
ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala 700 705 710	2403

GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
G TG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT GAT Phe Lys Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp 895 900 905	2979
ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG GTG Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val 910 915 920	3027
TGAGGCCCGG GGAGGCGCCC ACCTGCCAG TTAGCCGGC CAAGGACACT GATGGGTCT GCTGCTCGGG AAGGCCTGAG GGAAGCCCAC CCGCCCCAGA GACTGCCAC CCTGGGCCTC CCGTCCGT	3087 3147 3155

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 922 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser  
1 5 10 15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val  
20 25 30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln  
35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser  
50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu  
65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro  
85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly  
100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr  
115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr  
130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp  
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Met Leu Asn Met  
225 230 235 240

Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly  
245 250 255

Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile  
260 265 270

Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val  
275 280 285

Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro  
290 295 300

Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu  
305 310 315 320

Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly  
325 330 335

Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser  
340 345 350

Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn  
355 360 365

Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly  
370 375 380

Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile  
385 390 395 400

Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser  
405 410 415

Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys  
420 425 430

Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg  
435 440 445

His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile  
450 455 460

Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala  
465 470 475 480

Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys  
485 490 495

Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met  
500 505 510

Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu  
515 520 525

Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys  
530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser  
545 550 555 560

Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met  
565 570 575

Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn  
580 585 590

Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp  
595 600 605

Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro  
610 615 620

Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala  
625 630 635 640

Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val  
645 650 655

Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu  
660 665 670

Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser  
675 680 685

Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg  
690 695 700

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His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala  
705 710 715 720

Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu  
725 730 735

Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu  
740 745 750

Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp  
755 760 765

Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe  
770 775 780

Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser  
785 790 795 800

Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val  
805 810 815

Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe  
820 825 830

Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met  
835 840 845

Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp  
850 855 860

Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe  
865 870 875 880

Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser  
885 890 895

Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn  
900 905 910

Leu Ser Asp Pro Ser Val Ser Thr Val Val  
915 920

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2540 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..2334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAC GAC CAC TTC ACT CCC ACC CCT GTC TCC TAC ACA GCC GGC TTC TAC  
Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly Phe Tyr  
1 5 10 15

48

CGC ATA CCC GTG CTG GGG CTG ACC ACC CGC ATG TCC ATC TAC TCG GAC

96

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Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr Ser Asp		
20 25 30		
AAG AGC ATC CAC CTG AGC TTC CTG CGC ACC GTG CCG CCC TAC TCC CAC		144
Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr Ser His		
35 40 45		
CAG TCC AGC GTG TGG TTT GAG ATG ATG CGT GTC TAC AGC TGG AAC CAC		192
Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp Asn His		
50 55 60		
ATC ATC CTG CTG GTC AGC GAC GAC CAC GAG GGC CGG GCG GCT CAG AAA		240
Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala Gln Lys		
65 70 75 80		
CGC CTG GAG ACG CTG CTG GAG GAG CGT GAG TCC AAG AGT AAA AAA AGG		288
Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys Lys Arg		
85 90 95		
AAC TAT GAA AAC CTC GAC CAA CTG TCC TAT GAC AAC AAG CGC GGA CCC		336
Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg Gly Pro		
100 105 110		
AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG AAC GTG ACG		384
Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr		
115 120 125		
GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC ATC ATC CTT		432
Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu		
130 135 140		
TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA GCC GCG ATG		480
Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met		
145 150 155 160		
CTG AAC ATG ACG GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC		528
Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe		
165 170 175		
AAG AGA GTG CTG ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC		576
Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg		
180 185 190		
GTG GAG TTC AAT GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC		624
Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile		
195 200 205		
ATG AAC CTG CAG AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC		672
Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly		
210 215 220		
ACC CAC GTC ATC CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG		720
Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu		
225 230 235 240		
ACA GAG AAG CCT CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG		768
Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val		
245 250 255		
ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT		816
Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp		
260 265 270		
GGG ACA TGC AAG GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG		864
Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys		
275 280 285		

GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC CCC CGC CAC Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His 290 295 300	912
ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG CTC ATC AAG Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys 305 310 315 320	960
CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG GTG GCA GAT Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp 325 330 335	1008
GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC AAG AAG GAG Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu 340 345 350	1056
TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA GAC ATG ATC Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile 355 360 365	1104
GTG GCG CCG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC ATC GAG TTT Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe 370 375 380	1152
TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC AAG AAG GAG Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu 385 390 395 400	1200
ATT CCC CCG AGC ACG CTG GAC TCG TTC ATG CAG CCG TTC CAG AGC ACA Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr 405 410 415	1248
CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GCC GTG ATG CTG Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu 420 425 430	1296
TAC CTG CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG GTG AAC AGC Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser 435 440 445	1344
GAG GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GCC ATG TGG TTC Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe 450 455 460	1392
TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC GCC CCC AGA Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg 465 470 475 480	1440
AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC TTT GCC ATG Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met 485 490 495	1488
ATC ATC GTG GCC TCC TAC ACC GCC AAC CTG GCG GCC TTC CTG GTG CTG Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu 500 505 510	1536
GAC CGG CCG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT CGG CTG AGG Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg 515 520 525	1584
AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG AGC TCC GTG Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val 530 535 540	1632
GAT ATC TAC TTC CGG CGC CAG GTG GAG CTG AGC ACC ATG TAC CGG CAT Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His 545 550 555 560	1680

ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val 565 570 575	1728
AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu 580 585 590	1776
TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe 595 600 605	1824
TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys 610 615 620	1872
CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met 625 630 635 640	1920
GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg 645 650 655	1968
AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe 660 665 670	2016
ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile 675 680 685	2064
GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln 690 695 700	2112
CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg 705 710 715 720	2160
AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg 725 730 735	2208
GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser 740 745 750	2256
AAA GAC ACG CAG TAC CAT CCC ACT GAT ATC ACG GGC CCG CTC AAC CTC Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu 755 760 765	2304
TCA GAT CCC TCG GTC AGC ACC GTG GTG TGAGGCCCGG GGAGGCGCCC Ser Asp Pro Ser Val Ser Thr Val Val 770 775	2351
ACCTGCCAG TTAGCCCCGGC CAAGGACACT GATGGGTCT GCTGCTCGGG AAGGCCTGAG	2411
GGAAGCCAC CCGCCCCAGA GACTGCCAC CCTGGGCCTC CCGTCCGTCC GCCCGCCAC	2471
CCCGCTGCCCT GGCGGGCAGC CCCTGCTGGA CCAAGGTGCG GACCGGAGCG GCTGAGGACG	2531
GGGCAGAGC	2540

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 777 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly Phe Tyr  
1 5 10 15

Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr Ser Asp  
20 25 30

Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr Ser His  
35 40 45

Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp Asn His  
50 55 60

Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala Gln Lys  
65 70 75 80

Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys Lys Arg  
85 90 95

Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg Gly Pro  
100 105 110

Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr  
115 120 125

Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu  
130 135 140

Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met  
145 150 155 160

Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe  
165 170 175

Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg  
180 185 190

Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile  
195 200 205

Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly  
210 215 220

Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu  
225 230 235 240

Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val  
245 250 255

Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp  
260 265 270

Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys  
275 280 285

Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His  
290 295 300

Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys

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305                   310                   315                   320  
Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp  
325                   330                   335  
Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu  
340                   345                   350  
Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile  
355                   360                   365  
  
Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe  
370                   375                   380  
Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu  
385                   390                   395                   400  
Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr  
405                   410                   415  
Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu  
420                   425                   430  
Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser  
435                   440                   445  
Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe  
450                   455                   460  
Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg  
465                   470                   475                   480  
Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met  
485                   490                   495  
Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu  
500                   505                   510  
Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg  
515                   520                   525  
Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val  
530                   535                   540  
Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His  
545                   550                   555                   560  
Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val  
565                   570                   575  
Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu  
580                   585                   590  
Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe  
595                   600                   605  
Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys  
610                   615                   620  
Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met  
625                   630                   635                   640  
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg  
645                   650                   655  
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe

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660	665	670
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile		
675	680	685
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln		
690	695	700
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg		
705	710	715
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg		
725	730	735
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser		
740	745	750
Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu		
755	760	765
Ser Asp Pro Ser Val Ser Thr Val Val		
770	775	

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 595 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:

  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC	48
Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg	
1               5               10               15	
AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC	96
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe	
20              25              30	
ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC	144
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile	
35              40              45	
GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG	192
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln	
50              55              60	
CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA	240
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg	
65              70              75              80	
AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG	288
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg	
85              90              95	

GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC	336
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser	
100 105 110	
AAA GAC ACG CTG GCT CGG GAC TGT CTT CAA CCC TGC CCT GCA CCT TGG	384
Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp	
115 120 125	
GCA CGG GAG AGC GCC ACC CGC CCG CCC CCG CCC TCG CTC CGG GTG CGT	432
Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Ser Leu Arg Val Arg	
130 135 140	
GAC CGG CCC GCC ACC TTG TAC AGA ACC AGC ACT CCC AGG GCC CGA GCG	480
Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala	
145 150 155 160	
CGT GCC TTC CCC GTG CGC AGC CGC GCT CTG CCC CTC CGT CCC CAG GGT	528
Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly	
165 170 175	
GCA GGC GCG CAC CGC CCA ACC CCC ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA	583
Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp	
180 185 190	
AGGAATGTCA CG	595

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 191 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg	
1 5 10 15	
Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe	
20 25 30	
Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile	
35 40 45	
Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln	
50 55 60	
Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg	
65 70 75 80	
Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe Arg	
85 90 95	
Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser	
100 105 110	
Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp	
115 120 125	
Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Ser Leu Arg Val Arg	
130 135 140	
Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala	
145 150 155 160	

Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly  
165 170 175

Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp  
180 185 190

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 3935 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
      (A) NAME/KEY: CDS  
      (B) LOCATION: 262..3030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAAGCCGGGC	GTTCGGAGCT	GTGCCCGGCC	CCGCTTCAGC	ACCGCGGACA	GCGCCGGCCG	60
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC	120
CCGGGACCGC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCGGGGCCG	GGCGAGCGCA	180
GGACGGCCCG	GAAGCCCCGC	GGGGGATGCG	CCGAGGGCCC	CGCGTTCGCG	CCGCGCAGAG	240
CCAGGCCCGC	GGCCCGAGCC	C ATG AGC ACC ATG CGC	CTG CTG ACG CTC	GCC		291
		Met Ser Thr Met Arg	Leu Leu Thr	Leu Ala		
		1	5	10		
CTG CTG TTC TCC TGC TCC GTC	GCC CGT	GCC GCG	TGC GAC	CCC AAG	ATC	339
Leu Leu Phe Ser Cys Ser Val	Ala Arg	Ala Ala	Cys Asp	Pro Lys	Ile	
15	20	25				
GTC AAC ATT GGC GCG GTG CTG AGC ACG	CGG AAG	CAC GAG	CAG ATG	TTC		387
Val Asn Ile Gly Ala Val Leu Ser	Thr Arg	Lys His	Glu Gln	Met Phe		
30	35	40				
CGC GAG GCC GTG AAC CAG	GCC AAC	AAG CGG	CAC GGC	TCC TGG	AAG ATT	435
Arg Glu Ala Val Asn Gln Ala	Asn Lys	Arg His	Gly Ser	Trp Lys	Ile	
45	50	55				
CAG CTC AAT GCC ACC TCC GTC	ACG CAC	AAG CCC	AAC GCC	ATC CAG	ATG	483
Gln Leu Asn Ala Thr Ser Val	Thr His	Lys Pro	Asn Ala	Ile Gln	Met	
60	65	70				
GCT CTG TCG GTG TGC GAG	GAC CTC ATC	TCC AGC CAG	GTC TAC	GCC ATC		531
Ala Leu Ser Val Cys Glu Asp	Leu Ile Ser	Ser Gln	Val Tyr	Ala Ile		
75	80	85	90			
CTA GTT AGC CAT CCA CCT ACC CCC	AAC GAC	CAC TTC	ACT CCC	ACC CCT		579
Leu Val Ser His Pro Pro Thr	Pro Asn Asp	His Phe	Thr Pro	Thr Pro		
95	100	105				
GTC TCC TAC ACA GCC GGC	TTC TAC CGC	ATA CCC GTG	CTG GGG	CTG ACC		627
Val Ser Tyr Thr Ala Gly Phe	Tyr Arg Ile	Pro Val	Leu Gly	Leu Thr		
110	115	120				
ACC CGC ATG TCC ATC TAC TCG GAC	AAG AGC ATC CAC	CTG AGC	TTC CTG			675
Thr Arg Met Ser Ile Tyr Ser	Asp Lys Ser	Ile His	Leu Ser	Phe Leu		

	125	130	135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	140	145	150	723
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	155	160	165	771
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	175	180	185	819
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	190	195	200	867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	205	210	215	915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala	220	225	230	963
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly	235	240	245	1011
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile	255	260	265	1059
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser	270	275	280	1107
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys	285	290	295	1155
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile	300	305	310	1203
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr	315	320	325	1251
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg	335	340	345	1299
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val	350	355	360	1347
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys	365	370	375	1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met	380	385	390	1443

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TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr 395 400 405 410	1491
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val 415 420 425	1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr 430 435 440	1587
TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe 445 450 455	1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr 460 465 470	1683
GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val 475 480 485 490	1731
AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu 495 500 505	1779
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu 510 515 520	1827
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu 525 530 535	1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe 540 545 550	1923
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val 555 560 565 570	1971
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe 575 580 585	2019
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr 590 595 600	2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly 605 610 615	2115
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met 620 625 630	2163
GTC TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn 635 640 645 650	2211
CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly 655 660 665	2259

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ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala 670 675 680	2307
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu 685 690 695	2355
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala 700 705 710	2403
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile 715 720 725 730	2451
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu 735 740 745	2499
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met 750 755 760	2547
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys 765 770 775	2595
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CCG Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg 780 785 790	2643
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe 795 800 805 810	2691
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala 815 820 825	2739
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp 830 835 840	2787
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp 845 850 855	2835
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro 860 865 870	2883
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser 875 880 885 890	2931
TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT GAT Phe Lys Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp 895 900 905	2979
ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG GTG Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val 910 915 920	3027
TGAGGCCCCC GGAGGCCAG ACCTGCCAG TTAGCCGGC CAAGGACACT GATGGGTCTC	3087
GCTGCTCGGG AAGGCCTGAG GGAAGCCCCAC CCGCCCCAGA GACTGCCAC CCTGGGCCCTC	3147

CCGTCCGTCC	GCCCCCCCAC	CCCGCTGCCT	GGCGGGCAGC	CCCTGCTGGA	CCAAGGTGCG	3207
GACCGGAGCG	GCTGAGGACG	GGGCAGAGCT	GAGTCGGCTG	GGCAGGGCCG	CAGGGCGCTC	3267
CGGCAGAGGC	AGGCCCTGG	GGTCTCTGAG	CAGTGGGGAG	CGGGGGCTAA	CTGCCCCCAG	3327
CGGGAGGGC	TTGGAGCAGA	GACGGCAGCC	CCATCCTTCC	CGCAGCACCA	GCCTGAGCCA	3387
CAGTGGGGCC	CATGGCCCCA	GCTGGCTGGG	TCGCCCCCTCC	TCGGGCGCCT	GCGCTCCTCT	3447
GCAGCCTGAG	CTCCACCCCTC	CCCTCTTCTT	GCGGCACCGC	CCACCAAACA	CCCCGTCTGC	3507
CCCTTGACGC	CACACGCCGG	GGCTGGCGCT	GCCCTCCCCC	ACGGCCGTCC	CTGACTTCCC	3567
AGCTGGCAGC	GCCTCCCGCC	GCCTCGGGCC	GCCTCCTCCA	GAATCGAGAG	GGCTGAGCCC	3627
CTCCTCTCCT	CGTCCGGCCT	GCAGCACAGA	AGGGGGCCTC	CCCGGGGGTC	CCCGGACGCT	3687
GGCTCGGGAC	TGTCTTCAAC	CCTGCCCTGC	ACCTTGGGCA	CGGGAGAGCG	CCACCCGCC	3747
GCCCCCGCCC	TCGCTCCGGG	TGCGTGACCG	GCCC GCCACC	TTGTACAGAA	CCAGCACTCC	3807
CAGGGCCCGA	GCGCGTGCCT	TCCCCGTGCG	CAGCCGCGCT	CTGCCCCCTCC	GTCCCCAGGG	3867
TGCAGGGCGCG	CACCGCCCAA	CCCCCACCTC	CCGGTGTATG	CAGTGGTGAT	GCCTAAAGGA	3927
ATGTCACG						3935

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 922 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5				10						15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
								20		25		30			
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
								35		40		45			
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
								50		55		60			
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
								65		70		75		80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
								85		90		95			
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
								100		105		110			
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
								115		120		125			
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
								130		135		140			

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp  
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Met Leu Asn Met  
225 230 235 240

Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly  
245 250 255

Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile  
260 265 270

Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val  
275 280 285

Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro  
290 295 300

Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu  
305 310 315 320

Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly  
325 330 335

Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser  
340 345 350

Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn  
355 360 365

Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly  
370 375 380

Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile  
385 390 395 400

Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser  
405 410 415

Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys  
420 425 430

Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg  
435 440 445

His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile  
450 455 460

Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala  
465 470 475 480

Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys  
485 490 495

Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met

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500	505	510	
Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu			
515	520	525	
Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys			
530	535	540	
Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser			
545	550	555	560
Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met			
565	570		575
Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn			
580	585		590
Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp			
595	600		605
Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro			
610	615		620
Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala			
625	630		640
Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val			
645	650		655
Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu			
660	665		670
Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser			
675	680		685
Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg			
690	695		700
His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala			
705	710		720
Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu			
725	730		735
Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu			
740	745		750
Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp			
755	760		765
Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe			
770	775		780
Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser			
785	790		800
Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val			
805	810		815
Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe			
820	825		830
Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met			
835	840		845
Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp			

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850	855	860
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Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala Thr Phe	865	870 875 880
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Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser	885	890 895
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Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn	900	905 910
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Leu Ser Asp Pro Ser Val Ser Thr Val Val	915	920
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(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3211 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 262..3192

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala	291
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	339
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	387
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	435
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579

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Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro		
95	100	105
GTC TCC TAC ACA GCA GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC		627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr		
110	115	120
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG		675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu		
125	130	135
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG		723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met		
140	145	150
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC		771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp		
155	160	165
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG		819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu		
175	180	185
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG		867
Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys		
190	195	200
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC		915
Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val		
205	210	215
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA		963
Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala		
220	225	230
GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC GTG TGG CTG GTC GGC		1011
Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly		
235	240	245
GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC GCC CCA GAC GGC ATC		1059
Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile		
255	260	265
CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG TCG GCC CAC ATC AGC		1107
Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser		
270	275	280
GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC GAG CTC CTC GAG AAG		1155
Asp Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys		
285	290	295
GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG GGC AAC ACC AAC ATC		1203
Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile		
300	305	310
TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT		1251
Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr		
315	320	325
GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG		1299
Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg		
335	340	345
AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG		1347
Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val		

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	350	355	360	
CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys	365	370	375	1395
ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met	380	385	390	1443
TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr	395	400	405	1491
GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val	415	420	425	1539
AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr	430	435	440	1587
TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe	445	450	455	1635
TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr	460	465	470	1683
GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val	475	480	485	1731
AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu	495	500	505	1779
AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu	510	515	520	1827
CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu	525	530	535	1875
ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe	540	545	550	1923
ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val	555	560	565	1971
CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe	575	580	585	2019
GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr	590	595	600	2067
CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly	605	610	615	2115
ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG				2163

Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met		
620 625 630		
GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC		2211
Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn		
635 640 645 650		
CTG GCG GCC TTC CTG GTG CTG GAC CCG CCG GAG GAG CGC ATC ACG GGC		2259
Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly		
655 660 665		
ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC		2307
Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala		
670 675 680		
ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CCG CGC CAG GTG GAG		2355
Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu		
685 690 695		
CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG		2403
Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala		
700 705 710		
GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC		2451
Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile		
715 720 725 730		
TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG		2499
Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu		
735 740 745		
GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG		2547
Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met		
750 755 760		
CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG		2595
Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys		
765 770 775		
TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG		2643
Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg		
780 785 790		
TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT		2691
Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe		
795 800 805 810		
GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC		2739
Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala		
815 820 825		
GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT		2787
Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp		
830 835 840		
GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG		2835
Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp		
845 850 855		
CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT		2883
Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro		
860 865 870		
AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC		2931
Lys Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser		
875 880 885 890		

TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT CTT Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu 895 900 905	2979
CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG CCC Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro 910 915 920	3027
CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA ACC Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr 925 930 935	3075
AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC GCT Ser Thr Pro Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala 940 945 950	3123
CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC ACC Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr 955 960 965 970	3171
TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA CG Ser Arg Cys Met Gln Trp 975	3211

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 976 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser 1 5 10 15
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val 20 25 30
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln 35 40 45
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser 50 55 60
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu 65 70 75 80
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro 85 90 95
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly 100 105 110
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr 115 120 125
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr 130 135 140
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp 145 150 155 160
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala

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165	170	175
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu 180	185	190
Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu 195	200	205
Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser 210	215	220
Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met 225	230	235
Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly 245	250	255
Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile 260	265	270
Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp Ala Val Gly Val Val 275	280	285
Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro 290	295	300
Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu 305	310	315
Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly 325	330	335
Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser 340	345	350
Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn 355	360	365
Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly 370	375	380
Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile 385	390	395
Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser 405	410	415
Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys 420	425	430
Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg 435	440	445
His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile 450	455	460
Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala 465	470	475
Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys 485	490	495
Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met 500	505	510
Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu 515		

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515

520

525

Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys  
 530 535 540

Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser  
 545 550 555 560

Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val Met  
 565 570 575

Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn  
 580 585 590

Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp  
 595 600 605

Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro  
 610 615 620

Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala  
 625 630 635 640

Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val  
 645 650 655

Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu  
 660 665 670

Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser  
 675 680 685

Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg  
 690 695 700

His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala  
 705 710 715 720

Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu  
 725 730 735

Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu  
 740 745 750

Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp  
 755 760 765

Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe  
 770 775 780

Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser  
 785 790 795 800

Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val  
 805 810 815

Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe  
 820 825 830

Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met  
 835 840 845

Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp  
 850 855 860

Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe

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865	870	875	880
Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser		Phe Lys Arg Arg Arg Ser	
885		890	895
Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro			
900	905		910
Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val			
915	920	925	
Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg			
930	935	940	
Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln			
945	950	955	960
Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp			
965	970	975	

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4361 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 262..3141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala	291
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	339
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	387
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	435
45 50 55	

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CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	579
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	627
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	675
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	723
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	771
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	819
175 180 185	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG Arg Glu Ser Lys Ser Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu	867
190 195 200	
TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe	915
205 210 215	
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu	963
220 225 230	
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala	1011
235 240 245 250	
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr	1059
255 260 265	
GTG TGG CTG GTC GGC GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr	1107
270 275 280	
GCC CCA GAC GGC ATC CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu	1155
285 290 295	
TCG GCC CAC ATC AGC GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC Ser Ala His Ile Ser Asp Ala Val Gly Val Val Ala Gln Ala Val His	1203
300 305 310	
GAG CTC CTC GAG AAG GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val	1251
315 320 325 330	

GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu 335 340 345	1299
ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn 350 355 360	1347
GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln 365 370 375	1395
AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile 380 385 390	1443
CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro 395 400 405 410	1491
CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln 415 420 425	1539
GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys 430 435 440	1587
GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr 445 450 455	1635
GGG CCC AAC GAC ACG TCG CCG GGC AGC CCA CCC CGC CAC ACG GTG CCT CAG Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln 460 465 470	1683
TGT TGC TAC GGC TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC Cys Cys Tyr Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr 475 480 485 490	1731
ATG AAC TTC ACC TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly 495 500 505	1779
ACA CAG GAG CGG GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met 510 515 520	1827
ATG GGC GAG CTG CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu 525 530 535	1875
ACC ATA AAC AAC GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe 540 545 550	1923
AAG TAC CAG GGC CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser 555 560 565 570	1971
ACG CTG GAC TCG TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu 575 580 585	2019
GTC GGG CTG TCG GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp 590 595 600	2067

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CGC TTC AGC CCC TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu 605 610 615	2115
GAG GAC GCA CTG ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val 620 625 630	2163
CTG CTC AAC TCC GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala 635 640 645 650	2211
CGC ATC CTG GGC ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala 655 660 665	2259
TCC TAC ACC GCC AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG Ser Tyr Thr Ala Asn Leu Ala Phe Leu Val Leu Asp Arg Pro Glu 670 675 680	2307
GAG CGC ATC ACG GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp 685 690 695	2355
AAG TTT ATC TAC GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe 700 705 710	2403
CGG CGC CAG GTG GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His 715 720 725 730	2451
AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG Asn Tyr Glu Ser Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys 735 740 745	2499
CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser 750 755 760	2547
CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly 765 770 775	2595
TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser 780 785 790	2643
CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp 795 800 805 810	2691
AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro 815 820 825	2739
GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala 830 835 840	2787
GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr 845 850 855	2835
AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala 860 865 870	2883

3' C3' C3'

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GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg 875 880 885 890	2931
GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser 895 900 905	2979
ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC Thr Leu Ala Ser Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser 910 915 920	3027
ACC GGG GGT GGA CGC GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG Thr Gly Gly Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu 925 930 935	3075
CCG CGA CGC GCT ATT GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser 940 945 950	3123
CGT CAT AGG GAG AGC TGAGACTCCC CGCCCGCCCT CCTCTGCCCT CTCCCCCGCA Arg His Arg Glu Ser 955 960	3178
GACAGACAGA CAGACGGACG GGACAGCGGC CCGGCCACAG CAGAGCCCCG GAGCACACG GGGTCGGGG AGGAGCACCC CCAGCCTCCC CCAGGCTGCG CCTGCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC GTCCCCGCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTTCT ATTTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCCGC TCAACCTCTC AGATCCCTCG GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCACCTG CCCAGTTAGC CCGGCCAAGG ACACTGATGG GTCCTGCTGC TCGGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG CCCACCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCGC TGCCTGGCGG GCAGCCCCCTG CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGCA GAGCTGAGTC GGCTGGGCAG GGCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG GCTAACTGCC CCCAGGGGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG CACCAGCCTG AGCCACAGTG GGGCCATGG CCCAGCTGG CTGGGTCGCC CCTCCTCGGG CGCTCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCCTC TTCTTGCAGC ACCGCCACC AAACACCCCG TCTGCCCTT GACGCCACAC GCCGGGCTG GCGCTGCCCT CCCACCGGC CGTCCCTGAC TTCCCAGCTG GCAGCGCCTC CCGCCGCCCTC GGGCCGCCCTC CTCCAGAAC GAGAGGGCTG AGCCCCCTCCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG GCCTCCCCGG GGGTCCCCGG ACGCTGGCTC GGGACTGTCT TCAACCTGC CCTGCACCTT GGGCACGGGA GAGGCCACC CGCCCGCCCC CGCCCTCGCT CGGGTGCCT GACCGGCCCG CCACCTTGTA CAGAACCAAGC ACTCCCAGGG CCCGAGCGCG TGCCTCCCC GTGCGCAGCC GCGCTCTGCC CCTCCGTCCC CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCGGT GTATGCAGTG GTGATGCCTA AAGGAATGTC ACG	3238 3298 3358 3418 3478 3538 3598 3658 3718 3778 3838 3898 3958 4018 4078 4138 4198 4258 4318 4361

(2) INFORMATION FOR SEQ ID NO:24:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 959 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

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Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
 1           5          10          15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
 20          25          30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
 35          40          45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
 50          55          60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
 65          70          75          80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
 85          90          95

Thr Pro Asn Asp His Phe Thr Pro Val Ser Tyr Thr Ala Gly
100          105         110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
115          120         125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
130          135         140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
145          150         155         160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
165          170         175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Arg Glu Ser Lys Ser Lys
180          185         190

Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg
195          200         205

Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn
210          215         220

Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile
225          230         235         240

Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala
245          250         255

Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu
260          265         270

Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu
275          280         285

Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp
290          295         300

Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu

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305	310	315	320
Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp			
325		330	335
Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala			
340	345		350
Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys			
355		360	365
Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln			
370	375		380
Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile			
385	390	395	400
Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser			
405		410	415
Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val			
420	425		430
Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn			
435	440	445	
Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser			
450	455	460	
Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys			
465	470	475	480
Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu			
485		490	495
Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn			
500	505		510
Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser			
515	520	525	
Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg			
530	535	540	
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr			
545	550	555	560
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met			
565		570	575
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His			
580	585		590
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly			
595	600	605	
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu			
610	615	620	
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile			
625	630	635	640
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val			
645		650	655
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu			

660	665	670
Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile		
675	680	685
Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr		
690	695	700
Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu		
705	710	715
Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala		
725	730	735
Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp		
740	745	750
Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val		
755	760	765
Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg		
770	775	780
Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser		
785	790	795
His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr		
805	810	815
Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu		
820	825	830
Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly		
835	840	845
Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala		
850	855	860
Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg		
865	870	875
Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys		
885	890	895
Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe		
900	905	910
Lys Arg Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg Gly		
915	920	925
Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu		
930	935	940
Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser		
945	950	955

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4157 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA

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## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..2937

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG	240
CCAGGCCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	
175 180 185	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG	867
Arg Glu Ser Lys Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu	
190 195 200	

TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe	915
205 210 215	
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu	963
220 225 230	
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala	1011
235 240 245 250	
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn	1059
255 260 265	
ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys	1107
270 275 280	
TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp	1155
285 290 295	
CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu	1203
300 305 310	
GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg	1251
315 320 325 330	
AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln	1299
335 340 345	
ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val	1347
350 355 360	
TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr	1395
365 370 375	
GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp	1443
380 385 390	
ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly	1491
395 400 405 410	
TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr	1539
415 420 425	
TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg	1587
430 435 440	
GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu	1635
445 450 455	
CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn	1683
460 465 470	

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GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly 475 480 485 490	1731
CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser 495 500 505	1779
TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser 510 515 520	1827
GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro 525 530 535	1875
TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu 540 545 550	1923
ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser 555 560 565 570	1971
GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly 575 580 585	2019
ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala 590 595 600	2067
AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr 605 610 615	2115
GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr 620 625 630	2163
GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val 635 640 645 650	2211
GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser 655 660 665	2259
GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe 670 675 680	2307
ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp 685 690 695	2355
CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly 700 705 710	2403
ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu 715 720 725 730	2451
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val 735 740 745	2499

CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr 750 755 760	2547
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val 765 770 775	2595
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys 780 785 790	2643
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val 795 800 805 810	2691
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp 815 820 825	2739
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser 830 835 840	2787
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly 845 850 855	2835
CGC GGT GCT TTG CAA AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT Arg Gly Ala Leu Gln Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala 860 865 870	2883
ATT GAG AGG GAG GAG GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG Ile Glu Arg Glu Glu Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu 875 880 885 890	2931
AGC TGAGACTCCC CGCCCGCCCT CCTCTGCCCT CTCCCCCGCA GACAGACAGA Ser	2984
CAGACGGACG GGACAGCGGC CGGGCCCACG CAGAGCCCCG GAGCACCAACG GGGTCGGGG AGGAGCACCC CCAGCCTCCC CCAGGCTGCG CCTGCCGCC CGCCGGTTGG CCGGCTGGCC GGTCCACCCC GTCCCGGCC CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTCCT ATTTGCAGC AGTACCATCC CACTGATATC ACGGGCCCGC TCAACCTCTC AGATCCCTCG GTCAGCACCG TGGTGTGAGG CCCCCGGAGG CGCCCACCTG CCCAGTTAGC CCGGCCAAGG ACACTGATGG GTCCTGCTGC TCGGGAAAGC CTGAGGGAAAG CCCACCCGCC CCAGAGACTG CCCACCCCTGG GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCCTGGCGG GCAGCCCTG CTGGACCAAG GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG GGCGCAGGG CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG GCTAACTGCC CCCAGGCGGA GGGGCTTGGA GCAGAGACGG CAGCCCCATC CTTCCCGCAG CACCAGCCTG AGCCACAGTG GGGCCATGG CCCAGCTGG CTGGTGCCTC CCTCCTCGGG CGCCTGCGCT CCTCTGCAGC CTGAGCTCCA CCCTCCCTC TTCTTGCCTC ACCGCCCAAC AACACCCCCG TCTGCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCACGGC CGTCCCTGAC TTCCAGCTG GCAGCGCCTC CGGCCGCCTC GGGCCGCCTC	3044 3104 3164 3224 3284 3344 3404 3464 3524 3584 3644 3704 3764 3824

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CTCCAGAAC	GAGAGGGCTG	AGCCCCCTCCT	CTCCTCGTCC	GGCCTGCAGC	ACAGAAAGGG	3884
GCCTCCCCGG	GGGTCCCCGG	ACGCTGGCTC	GGGACTGTCT	TCAACCCTGC	CCTGCACCTT	3944
GGGCACGGGA	GAGCGCCACC	CGCCCCGCCC	CGCCCTCGCT	CCGGGTGCGT	GACCGGCCG	4004
CCACCTTGTA	CAGAACCAAGC	ACTCCCAGGG	CCCGAGCGCG	TGCCTTCCCC	GTGCGCAGCC	4064
GCGCTCTGCC	CCTCCGTCCC	CAGGGTGCAG	GCGCGCACCG	CCCAACCCCC	ACCTCCCGGT	4124
GTATGCAGTG	GTGATGCCTA	AAGGAATGTC	ACG			4157

## (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 891 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5				10						15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
				20				25					30		
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
				35			40				45				
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
				50			55				60				
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
				65			70				75			80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
				85			90				95				
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
				100			105				110				
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
				115			120				125				
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
				130			135				140				
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
				145			150				155			160	
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
				165			170				175				
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys
				180			185				190				
Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	Ser	Tyr	Asp	Asn	Lys	Arg
				195			200				205				
Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn
				210			215				220				
Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile

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225	230	235	240												
Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala
				245				250				255			
Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro
	260				265						270				
Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr
	275				280				285						
Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr
	290		295					300							
Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	Val	Gln	Val	Gly	Ile	Tyr
	305			310				315			320				
Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	Lys	Ile	Ile	Trp	Pro	Gly
		325				330			335						
Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	Met	Ser	Thr	Arg	Leu	Lys
	340			345				350							
Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	Tyr	Val	Lys	Pro	Thr	Leu
	355				360				365						
Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val
	370			375				380							
Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro
	385			390				395			400				
Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Leu
		405				410			415						
Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val
		420				425			430						
Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys
	435				440				445						
Lys	Glu	Trp	Asn	Gly	Met	Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp
	450			455				460							
Met	Ile	Val	Ala	Pro	Leu	Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile
	465				470			475			480				
Glu	Phe	Ser	Lys	Pro	Phe	Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys
	485				490			495							
Lys	Glu	Ile	Pro	Arg	Ser	Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln
	500				505			510							
Ser	Thr	Leu	Trp	Leu	Leu	Val	Gly	Leu	Ser	Val	His	Val	Val	Ala	Val
	515				520			525							
Met	Leu	Tyr	Leu	Leu	Asp	Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val
	530				535			540							
Asn	Ser	Glu	Glu	Glu	Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	
	545				550				555				560		
Trp	Phe	Ser	Trp	Gly	Val	Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala
		565				570			575						
Pro	Arg	Ser	Phe	Ser	Ala	Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe

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580

585

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Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu  
 595 600 605  
 Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg  
 610 615 620  
 Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser  
 625 630 635 640  
 Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr  
 645 650 655  
 Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln  
 660 665 670  
 Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val  
 675 680 685  
 Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu  
 690 695 700  
 Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro  
 705 710 715 720  
 Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly  
 725 730 735  
 Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp  
 740 745 750  
 Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly  
 755 760 765  
 Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile  
 770 775 780  
 Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln  
 785 790 795 800  
 Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln  
 805 810 815  
 Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr  
 820 825 830  
 Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg  
 835 840 845  
 Ser Ser Lys Asp Thr Ser Thr Gly Gly Gly Arg Gly Ala Leu Gln Asn  
 850 855 860  
 Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu Gly  
 865 870 875 880  
 Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser  
 885 890

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3794 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: both

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 262..2889

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAAGCCGGGC	GTTCGGAGCT	GTGCCCGGCC	CCGCTTCAGC	ACCGCGGACA	GCGCCGGCCG	60
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC	120
CCGGGACCGC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCAGGGCCG	GGCGAGCGCA	180
GGACGGCCCC	GAAGCCCCGC	GGGGGATGCG	CCGAGGGCCC	CGCGTTCGCG	CCGCGCAGAG	240
CCAGGCCCGC	GGCCCGAGCC	C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC				291
		Met Ser Thr Met Arg Leu Leu Thr Leu Ala				
		1 5 10				
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC						339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile						
15 20 25						
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC						387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe						
30 35 40						
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT						435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile						
45 50 55						
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG						483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met						
60 65 70						
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC						531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile						
75 80 85 90						
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT						579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro						
95 100 105						
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC						627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr						
110 115 120						
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG						675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu						
125 130 135						
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG						723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met						
140 145 150						
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC						771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp						
155 160 165 170						
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG						819

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His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
				175				180						185		
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
				190				195					200			
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
				205				210				215				
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
				220			225				230					
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
				235			240			245			250			
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	AAC	ACC	AAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Asn	Thr	Asn	
				255			260			265						
ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	ATG	TCT	TCC	AAG	1107
Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	Met	Ser	Ser	Lys	
				270			275			280						
TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	GAG	GAT	GGG	GAC	1155
Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	Glu	Asp	Gly	Asp	
				285			290			295						
CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	AAC	CGC	AAG	CTG	1203
Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	Asn	Arg	Lys	Leu	
				300			305			310						
GTG	CAA	GTG	GGC	ATC	TAC	AAT	GGC	ACC	CAC	GTC	ATC	CCT	AAT	GAC	AGG	1251
Val	Gln	Val	Gly	Ile	Tyr	Asn	Gly	Thr	His	Val	Ile	Pro	Asn	Asp	Arg	
				315			320			325			330			
AAG	ATC	ATC	TGG	CCA	GGC	GGA	GAG	ACA	GAG	AAG	CCT	CGA	GGG	TAC	CAG	1299
Lys	Ile	Ile	Trp	Pro	Gly	Gly	Glu	Thr	Glu	Lys	Pro	Arg	Gly	Tyr	Gln	
				335			340			345						
ATG	TCC	ACC	AGA	CTG	AAG	ATT	GTG	ACG	ATC	CAC	CAG	GAG	CCC	TTC	GTG	1347
Met	Ser	Thr	Arg	Leu	Lys	Ile	Val	Thr	Ile	His	Gln	Glu	Pro	Phe	Val	
				350			355			360						
TAC	GTC	AAG	CCC	ACG	CTG	AGT	GAT	GGG	ACA	TGC	AAG	GAG	GAG	TTC	ACA	1395
Tyr	Val	Lys	Pro	Thr	Leu	Ser	Asp	Gly	Thr	Cys	Lys	Glu	Glu	Phe	Thr	
				365			370			375						
GTC	AAC	GGC	GAC	CCA	GTC	AAG	AAG	GTG	ATC	TGC	ACC	GGG	CCC	AAC	GAC	1443
Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	Gly	Pro	Asn	Asp	
				380			385			390						
ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	TGT	TGC	TAC	GGC	1491
Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	Cys	Cys	Tyr	Gly	
				395			400			405			410			
TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	ATG	AAC	TTC	ACC	1539
Phe	Cys	Ile	Asp	Leu	Leu	Ile	Lys	Leu	Ala	Arg	Thr	Met	Asn	Phe	Thr	
				415			420			425						
TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	ACA	CAG	GAG	CGG	1587
Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	Thr	Gln	Glu	Arg	
				430			435			440						

GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu 445 450 455	1635
CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn 460 465 470	1683
GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly 475 480 485 490	1731
CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser 495 500 505	1779
TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser 510 515 520	1827
GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro 525 530 535	1875
TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu 540 545 550	1923
ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser 555 560 565 570	1971
GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly 575 580 585	2019
ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala 590 595 600	2067
AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr 605 610 615	2115
GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr 620 625 630	2163
GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val 635 640 645 650	2211
GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser 655 660 665	2259
GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe 670 675 680	2307
ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp 685 690 695	2355
CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly 700 705 710	2403

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ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu 715 720 725 730	2451
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val 735 740 745	2499
CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr 750 755 760	2547
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val 765 770 775	2595
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys 780 785 790	2643
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val 795 800 805 810	2691
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp 815 820 825	2739
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser 830 835 840	2787
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG TAC CAT CCC ACT Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr 845 850 855	2835
GAT ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG GTC AGC ACC GTG Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val 860 865 870	2883
GTG TGAGGCCCGGG GGAGGCGCCCC ACCTGCCAG TTAGCCGGC CAAGGACACT Val 875	2936
GATGGGTCCCT GCTGCTCGGG AAGGCCGTGAG GGAAGCCCAC CCGCCCCAGA GACTGCCAC	2996
CCTGGGCCTC CCGTCCGTCC GCCCCCCCAC CCCGCTGCCCT GGCGGGCAGC CCCTGCTGGA	3056
CCAAGGTGCG GACCGGAGCG GCTGAGGACG GGGCAGAGCT GAGTCGGCTG GGCAGGGCCG	3116
CAGGGCGCTC CGGCAGAGGC AGGCCCCCTGG GGTCTCTGAG CAGTGGGGAG CGGGGGCTAA	3176
CTGCCCTCAG GCGGAGGGGC TTGGAGCAGA GACGGCAGCC CCATCCTTCC CGCAGCACCA	3236
GCCTGAGCCA CAGTGGGGCC CATGCCCTCA GCTGGCTGGG TCGCCCCCTCC TCAGGGCGCCT	3296
GCGCTCCTCT GCAGCCTGAG CTCCACCCTC CCCTCTTCTT GCGGCACCGC CCACCAAACA	3356
CCCCGTCTGC CCCTTGACGC CACACGCCGG GGCTGGCGCT GCCCTCCCCC ACGGCCGTCC	3416
CTGACTTCCC AGCTGGCAGC GCCTCCCGCC GCCTCGGGCC GCCTCCTCCA GAATCGAGAG	3476
GGCTGAGCCC CTCCCTCTCCT CGTCCGGCCT GCAGCACAGA AGGGGGCCTC CCCGGGGGTC	3536
CCCGGACGCT GGCTCGGGAC TGTCTTCAAC CCTGCCCTGC ACCTTGGGCA CGGGAGAGCG	3596
CCACCCGCCCGGG GCCCCCGCCCC TCGCTCCGGG TGCGTGTGACCG GCCCGCCACC TTGTACAGAA	3656

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CCAGCACTCC CAGGGCCCGA GCGCGTGCCT TCCCCGTGCG CAGCCGCGCT CTGCCCTCC	3716
GTCCCCAGGG TGCAGGCGCG CACCGCCCAA CCCCCACCTC CCGGTGTATG CAGTGGTGAT	3776
GCCTAAAGGA ATGTCACG	3794

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 875 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	
165 170 175	
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys	
180 185 190	
Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg	
195 200 205	
Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn	
210 215 220	
Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile	
225 230 235 240	
Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala	
245 250 255	
Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro	

260	265	270
Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr		
275	280	285
Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr		
290	295	300
Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr		
305	310	315
Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly		
325	330	335
Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys		
340	345	350
Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu		
355	360	365
Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val		
370	375	380
Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro		
385	390	395
Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu		
405	410	415
Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val		
420	425	430
Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys		
435	440	445
Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp		
450	455	460
Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile		
465	470	475
480		
Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys		
485	490	495
Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln		
500	505	510
Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val		
515	520	525
Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val		
530	535	540
Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met		
545	550	555
560		
Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala		
565	570	575
Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe		
580	585	590
Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu		
595	600	605
Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg		
610	615	620

Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser  
625 630 635 640

Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr  
645 650 655

Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln  
660 665 670

Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val  
675 680 685

Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu  
690 695 700

Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro  
705 710 715 720

Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly  
725 730 735

Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp  
740 745 750

Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly  
755 760 765

Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile  
770 775 780

Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln  
785 790 795 800

Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln  
805 810 815

Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr  
820 825 830

Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg  
835 840 845

Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu  
850 855 860

Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val  
865 870 875

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4094 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 262..2874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

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CAAGCCGGGC	GTTCGGAGCT	GTGCCGGGCC	CCGCTTCAGC	ACCGCGGACA	GCGCCGGCCG	60
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC	120
CCGGGACCGC	CGCTCCGGGG	GAGACGTGGC	GTCCGCAGCC	CGCGGGGCCG	GGCGAGCGCA	180
GGACGGCCCG	GAAGCCCCGC	GGGGGATGCG	CCGAGGGCCC	CGCGTTCGCG	CCGCGCAGAG	240
CCAGGCCCGC	GGCCCGAGCC	C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	Met Ser Thr Met Arg Leu Leu Thr Leu Ala			291
		1	5		10	
CTG CTG TTC TCC TGC TCC GTC	GCC CGT GCG TGC GAC CCC AAG ATC	339				
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	15 20 25					
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	387				
30 35 40						
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	435				
45 50 55						
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	483				
60 65 70						
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	531				
75 80 85 90						
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	579				
95 100 105						
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	627				
110 115 120						
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	675				
125 130 135						
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	723				
140 145 150						
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	771				
155 160 165 170						
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	819				
175 180 185						
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG	Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys	867				
190 195 200						
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC	Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val	915				
205 210 215						
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA	Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala	963				
220 225 230						

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GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC ATC TGG AAG ACC GGG Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly 235 240 245 250	1011
CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT GCG GAT GGG GTG Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val 255 260 265	1059
ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG AAG TTC GCC AAC Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn 270 275 280	1107
TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG CAA GTG GGC ATC Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile 285 290 295	1155
TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG ATC ATC TGG CCA Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro 300 305 310	1203
GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG TCC ACC AGA CTG Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu 315 320 325 330	1251
AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr 335 340 345	1299
CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC AAC GGC GAC CCA Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro 350 355 360	1347
GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser 365 370 375	1395
CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu 380 385 390	1443
CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu 395 400 405 410	1491
GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn 415 420 425	1539
AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala 430 435 440	1587
GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr 445 450 455	1635
ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val 460 465 470	1683
AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC ATG CAG CCG TTC Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe 475 480 485 490	1731
CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GCC Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala	1779

495	500	505	
GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys 510	515	520	1827
GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GCC Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala 525	530	535	1875
ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly 540	545	550	1923
GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly 555	560	565	1971
TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC CTG GCG GCC TTC Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Phe 575	580	585	2019
CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro 590	595	600	2067
CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln 605	610	615	2115
AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG GAG CTG AGC ACC ATG Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met 620	625	630	2163
TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile 635	640	645	2211
CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala 655	660	665	2259
GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly 670	675	680	2307
GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser 685	690	695	2355
CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn 700	705	710	2403
GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys 715	720	725	2451
GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala 735	740	745	2499
GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu 750	755	760	2547
ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG			2595

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Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys		
765 770 775		
CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG	2643	
Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu		
780 785 790		
CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC	2691	
Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala		
795 800 805 810		
ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT	2739	
Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg		
815 820 825		
AGG TCC TCC AAA GAC ACG AGC ACC GGG GGT GGA CGC GGT GCT TTG CAA	2787	
Arg Ser Ser Lys Asp Thr Ser Thr Gly Gly Arg Gly Ala Leu Gln		
830 835 840		
AAC CAA AAA GAC ACA GTG CTG CCG CGA CGC GCT ATT GAG AGG GAG GAG	2835	
Asn Gln Lys Asp Thr Val Leu Pro Arg Arg Ala Ile Glu Arg Glu Glu		
845 850 855		
GGC CAG CTG CAG CTG TGT TCC CGT CAT AGG GAG AGC TGAGACTCCC	2881	
Gly Gln Leu Gln Leu Cys Ser Arg His Arg Glu Ser		
860 865 870		
CGCCCGCCCT CCTCTGCCCT CTCCCCCGCA GACAGACAGA CAGACGGACG GGACAGCGGC	2941	
CCGGCCCACG CAGAGCCCCG GAGCACACG GGGTCGGGG AGGAGCACCC CCAGCCTCCC	3001	
CCAGGCTGCG CCTGCCCGCC CGCCGGTTGG CCGGCTGCC GGTCCACCCC GTCCCGGCC	3061	
CGCGCGTGCC CCCAGCGTGG GGCTAACGGG CGCCTTGTCT GTGTATTTCT ATTTTGAGC	3121	
AGTACCATCC CACTGATATC ACGGGCCCCG TCAACCTCTC AGATCCCTCG GTCAGCACCG	3181	
TGGTGTGAGG CCCCCGGAGG CGCCCACCTG CCCAGTTAGC CCGGCCAAGG ACACTGATGG	3241	
GTCCTGCTGC TCAGGAAGGC CTGAGGGAAG CCCACCCGCC CCAGAGACTG CCCACCCCTGG	3301	
GCCTCCCGTC CGTCCGCCCG CCCACCCCGC TGCCTGCCGG GCAGCCCCCTG CTGGACCAAG	3361	
GTGCGGACCG GAGCGGCTGA GGACGGGGCA GAGCTGAGTC GGCTGGGCAG GGCGCAGGG	3421	
CGCTCCGGCA GAGGCAGGCC CCTGGGGTCT CTGAGCAGTG GGGAGCGGGG GCTAACTGCC	3481	
CCCAGGGGA GGGGCTTGGG GCAGAGACGG CAGCCCCATC CTTCCCGCAG CACCAGCTG	3541	
AGCCACAGTG GGGCCCCTGG CCCCAGCTGG CTGGGTGCC CCTCCTCGGG CGCCTGCGCT	3601	
CCTCTGCAGC CTGAGCTCCA CCCTCCCCCTC TTCTTGCAGG ACCGGCCACC AAACACCCCG	3661	
TCTGCCCTT GACGCCACAC GCCGGGGCTG GCGCTGCCCT CCCCCACGGC CGTCCCTGAC	3721	
TTCCCAAGCTG GCAGCGCCTC CGGCCGCCCTC GGGCCGCCCTC CTCCAGAATC GAGAGGGCTG	3781	
AGCCCCCTCT CTCCTCGTCC GGCCTGCAGC ACAGAAGGGG GCCTCCCCGG GGGTCCCCGG	3841	
ACGCTGGCTC GGGACTGTCT TCAACCCCTGC CCTGCACCTT GGGCACGGGA GAGGCCACC	3901	
CGCCCGCCCG CGCCCTCGCT CGGGGTGCGT GACCGGGCCCG CCACCTTGTA CAGAACCGAC	3961	
ACTCCCAGGG CCCGAGCGCG TGCCCTCCCC GTGCGCAGCC GCGCTCTGCC CCTCCGTCCC	4021	
CAGGGTGCAG GCGCGCACCG CCCAACCCCC ACCTCCCCGT GTATGCAGTG GTGATGCCATA	4081	

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AAGGAATGTC ACG

4094

## (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 870 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1					5				10					15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
					20			25					30		
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
					35			40					45		
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
					50			55					60		
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
					65			70			75		80		
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
					85			90					95		
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
					100			105					110		
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
					115			120					125		
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
					130			135					140		
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
					145			150			155		160		
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
					165			170					175		
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ala	Glu
					180			185					190		
Lys	Val	Leu	Gln	Phe	Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu
					195			200					205		
Met	Glu	Ala	Lys	Glu	Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser
					210			215					220		
Glu	Asp	Asp	Ala	Ala	Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met
					225			230					235		240
Thr	Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val
					245			250					255		
Leu	Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe
					260			265					270		
Asn	Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu
					275			280					285		

Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val  
290 295 300

Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys  
305 310 315 320

Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His  
325 330 335

Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys  
340 345 350

Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys  
355 360 365

Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro  
370 375 380

Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg  
385 390 395 400

Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe  
405 410 415

Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly  
420 425 430

Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro  
435 440 445

Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro  
450 455 460

Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg  
465 470 475 480

Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu  
485 490 495

Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu  
500 505 510

Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu  
515 520 525

Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly  
530 535 540

Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser  
545 550 555 560

Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val  
565 570 575

Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro  
580 585 590

Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser  
595 600 605

Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr  
610 615 620

Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys  
625 630 635 640

His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn

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645

650

655

Lys	Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala
660								665							670
Ser	Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser
675							680								685
Gly	Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val
690							695					700			
Ser	Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu
705							710					715			720
Asp	Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala
725							730								735
Pro	Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val
740							745						750		
Ala	Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala
755							760						765		
Tyr	Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe
770							775					780			
Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly
785							790					795			800
Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	
805							810						815		
Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg	Arg	Ser	Ser	Lys	Asp	Thr
820							825						830		
Ser	Thr	Gly	Gly	Gly	Arg	Gly	Ala	Leu	Gln	Asn	Gln	Lys	Asp	Thr	Val
835							840						845		
Leu	Pro	Arg	Arg	Ala	Ile	Glu	Arg	Glu	Glu	Gly	Gln	Leu	Gln	Leu	Cys
850							855						860		
Ser	Arg	His	Arg	Glu	Ser										
865							870								

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3731 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 262..2826

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAAGCCGGGC	GTTCGGAGCT	GTGCCGGCC	CCGCTTCAGC	ACCGCGGACA	GCGCCGGCCG		60
CGTGGGGCTG	AGCGCCGAGC	CCCCGCGCAC	GCTTCAGCCC	CCCTTCCCTC	GGCCGACGTC		120

CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC Met Ser Thr Met Arg Leu Leu Thr Leu Ala 1 5 10	291
CTG CTG TTC TCC TGC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile 15 20 25	339
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe 30 35 40	387
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile 45 50 55	435
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met 60 65 70	483
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile 75 80 85 90	531
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro 95 100 105	579
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr 110 115 120	627
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu 125 130 135	675
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 140 145 150	723
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 155 160 165 170	771
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu 175 180 185	819
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 190 195 200	867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val 205 210 215	915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230	963
GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC ATC TGG AAG ACC GGG Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly 235 240 245 250	1011

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CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT GCG GAT GGG GTG Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val 255 260 265	1059
ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG AAG TTC GCC AAC Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn 270 275 280	1107
TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG CAA GTG GGC ATC Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile 285 290 295	1155
TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG ATC ATC TGG CCA Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro 300 305 310	1203
GGA GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG TCC ACC AGA CTG Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu 315 320 325 330	1251
AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr 335 340 345	1299
CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC AAC GGC GAC CCA Leu Ser Asp Gly Thr Cys Lys Glu Phe Thr Val Asn Gly Asp Pro 350 355 360	1347
GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC Val Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser 365 370 375	1395
CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu 380 385 390	1443
CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu 395 400 405 410	1491
GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn 415 420 425	1539
AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala 430 435 440	1587
GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr 445 450 455	1635
ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val 460 465 470	1683
AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC ATG CAG CCG TTC Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe 475 480 485 490	1731
CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GCC Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala 495 500 505	1779
GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys	1827

510	515	520	
GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GCC Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala 525	530	535	1875
ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly 540	545	550	1923
GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly 555	560	565	1971
TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC CTG GCG GCC TTC Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe 575	580	585	2019
CTG GTG CTG GAC CCG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro 590	595	600	2067
CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln 605	610	615	2115
AGC TCC GTG GAT ATC TAC TTC CCG CGC CAG GTG GAG CTG AGC ACC ATG Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met 620	625	630	2163
TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile 635	640	645	2211
CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala 655	660	665	2259
GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA Val Leu Glu Phe Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly 670	675	680	2307
GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser 685	690	695	2355
CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn 700	705	710	2403
GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys 715	720	725	2451
GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala 735	740	745	2499
GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu 750	755	760	2547
ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys 765	770	775	2595
CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTC TGG CGG AAG AAC CTG			2643

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Gln	Met	Gln	Leu	Ala	Phe	Ala	Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu		
780					785						790						
CAG	GAT	AGA	AAG	AGT	GGT	AGA	GCA	GAG	CCT	GAC	CCT	AAA	AAG	AAA	GCC	2691	
Gln	Asp	Arg	Lys	Ser	Gly	Arg	Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala		
795					800					805						810	
ACA	TTT	AGG	GCT	ATC	ACC	TCC	ACC	CTG	GCT	TCC	AGC	TTC	AAG	AGG	CGT	2739	
Thr	Phe	Arg	Ala	Ile	Thr	Ser	Thr	Leu	Ala	Ser	Ser	Phe	Lys	Arg	Arg		
	815							820					825				
AGG	TCC	TCC	AAA	GAC	ACG	CAG	TAC	CAT	CCC	ACT	GAT	ATC	ACG	GGC	CCG	2787	
Arg	Ser	Ser	Lys	Asp	Thr	Gln	Tyr	His	Pro	Thr	Asp	Ile	Thr	Gly	Pro		
	830							835					840				
CTC	AAC	CTC	TCA	GAT	CCC	TCG	GTC	AGC	ACC	GTG	GTG	TGAGGCC				2833	
Leu	Asn	Leu	Ser	Asp	Pro	Ser	Val	Ser	Thr	Val	Val						
	845						850				855						
GGAGGCC	ACCTGCC	AG	TTAGCC	GGC	CAAGG	AC	GACT	GAT	GGG	TCT	CCT	GCT	GTC	CGGG		2893	
AAGGC	C	TGAG	GGAAG	CCCAC	CCG	CCCC	CAGA	GA	CTG	CCCAC	CCT	GGG	CC	CGT	CCGT		2953
GCC	CC	AC	CCC	GTG	CC	GG	GGG	CAGC	CC	CTG	CTG	GA	CC	GG	AGCG		3013
GCT	GAG	GAC	GGG	CAGAG	G	AGT	CGG	CTG	GG	CAGGG	CC	AGG	CG	CG	AGAG		3073
AGG	CCC	CTG	GG	GGT	CT	CTG	AG	CAG	GGG	GGCTAA	CTG	CCCC	CA	GG	AGGG		3133
TTGG	GAG	CAGA	GAC	GGG	CAG	CC	ATC	CTT	CC	CGCAGCACCA	GC	CTGAG	CC	AGT	GGG		3193
CATGG	CCC	CCA	G	CTG	GG	CTG	GGG	TCG	CCC	CTCC	TC	GGG	CG	CT	CCT		3253
CTCC	AC	CC	CT	CT	CC	GC	GG	AC	CC	CC	CT	GC	CT	CC	TG		3313
CACAC	GCC	GG	CTG	GG	CG	CT	GC	CT	CC	AC	GG	CC	GT	CC	AG		3373
GC	CT	CC	GG	CC	GC	CT	CC	TC	CC	AC	GG	CC	GT	CC	AG		3433
CGT	CC	GG	CT	GC	CT	GC	AG	CA	CC	GG	GG	GT	CC	GG	AC		3493
TGT	CTT	CAAC	C	CTG	CC	CTG	GC	AC	CTT	GGG	CA	GGG	AG	AG	CG		3553
TCG	CT	CC	GG	GG	TG	CGT	GAC	CG	CC	GG	CC	AC	GC	AC	TC		3613
GCG	CG	TG	CC	CT	GC	CT	GC	GT	CC	CC	CC	CC	AG	GG	CG		3673
CAC	CG	CC	AA	CCC	CC	AC	CG	GT	GT	AT	GG	CC	GA	TC	AC		3731

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 854 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser  
1 5 10 15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val  
20 25 30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln  
35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser  
50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu  
65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro  
85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly  
100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr  
115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr  
130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp  
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu  
180 185 190

Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu  
195 200 205

Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser  
210 215 220

Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met  
225 230 235 240

Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val  
245 250 255

Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe  
260 265 270

Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu  
275 280 285

Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val  
290 295 300

Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys  
305 310 315 320

Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His  
325 330 335

Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys  
340 345 350

Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys  
355 360 365

Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro  
370 375 380

Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg

385                   390                   395                   400  
  
Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe  
405                   410                   415  
  
Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly  
420                   425                   430  
  
Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro  
435                   440                   445  
  
Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro  
450                   455                   460  
  
Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg  
465                   470                   475                   480  
  
Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu  
485                   490                   495  
  
Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu  
500                   505                   510  
  
Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu  
515                   520                   525  
  
Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly  
530                   535                   540  
  
Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser  
545                   550                   555                   560  
  
Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val  
565                   570                   575  
  
Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro  
580                   585                   590  
  
Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser  
595                   600                   605  
  
Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr  
610                   615                   620  
  
Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys  
625                   630                   635                   640  
  
His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn  
645                   650                   655  
  
Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala  
660                   665                   670  
  
Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser  
675                   680                   685  
  
Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val  
690                   695                   700  
  
Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu  
705                   710                   715                   720  
  
Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala  
725                   730                   735  
  
Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val

740

745

750

Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala  
755 760 765

Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe  
770 775 780

Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly  
785 790 795 800

Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr  
805 810 815

Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr  
820 825 830

Gln Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro  
835 840 845

Ser Val Ser Thr Val Val  
850

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3007 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..2988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG	240
CCAGGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	

CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met 60 65 70	483
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile 75 80 85 90	531
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro 95 100 105	579
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr 110 115 120	627
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu 125 130 135	675
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met 140 145 150	723
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp 155 160 165 170	771
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu 175 180 185	819
CGT GAG TCC AAG GCA GAG AAG GTG CTG CAG TTT GAC CCA GGG ACC AAG Arg Glu Ser Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys 190 195 200	867
AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG CTG GAG GCC CGG GTC Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val 205 210 215	915
ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC ACT GTA TAC CGC GCA Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala 220 225 230	963
GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC ATC TGG AAG ACC GGG Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly 235 240 245 250	1011
CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG TAT GCG GAT GGG GTG Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val 255 260 265	1059
ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC CGG AAG TTC GCC AAC Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn 270 275 280	1107
TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG GTG CAA GTG GGC ATC Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile 285 290 295	1155
TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG AAG ATC ATC TGG CCA Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro 300 305 310	1203
GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG ATG TCC ACC AGA CTG Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu 315 320 325 330	1251

AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG TAC GTC AAG CCC ACG Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr 335 340 345	1299
CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA GTC AAC GGC GAC CCA Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro 350 355 360	1347
GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC ACG TCG CCG GGC AGC Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser 365 370 375	1395
CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC TTT TGC ATC GAC CTG Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu 380 385 390	1443
CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC TAC GAG GTG CAC CTG Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu 395 400 405 410	1491
GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG GTG AAC AAC AGC AAC Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn 415 420 425	1539
AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG CTC AGC GGG CAG GCA Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala 430 435 440	1587
GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC GAG CGC GCG CAG TAC Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr 445 450 455	1635
ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC CTG ACT ATT CTG GTC Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val 460 465 470	1683
AAG AAG GAG ATT CCC CGG AGC ACG CTG GAC TCG TTC ATG CAG CCG TTC Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe 475 480 485 490	1731
CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG GTG CAC GTG GTG GCC Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala 495 500 505	1779
GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC TTC GGC CGG TTC AAG Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys 510 515 520	1827
GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG ACC CTG TCC TCG GGC Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala 525 530 535	1875
ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC GGC ATC GGG GAA GGC Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly 540 545 550	1923
GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC ATG GTG TGG GCC GGC Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly 555 560 565 570	1971
TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC AAC CTG GCG GCC TTC Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe 575 580 585	2019
CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG GGC ATC AAC GAC CCT Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro 590 595 600	2067

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CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC GCC ACG GTG AAG CAG Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln 605 610 615	2115
AGC TCC GTG GAT ATC TAC TTC CCG CGC CAG GTG GAG CTG AGC ACC ATG Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met 620 625 630	2153
TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT GCG GCG GAG GCC ATC Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile 635 640 645 650	2211
CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC ATC TGG GAC TCG GCG Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala 655 660 665	2259
GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC CTG GTG ACG ACT GGA Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly 670 675 680	2307
GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC ATG CGC AAA GAC AGC Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser 685 690 695	2355
CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC AAG TCC CAC GAG AAT Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn 700 705 710	2403
GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT CGG TAT CAG GAA TGT Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys 715 720 725 730	2451
GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT TTT GAG AAC ATG GCC Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala 735 740 745	2499
GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG GCC GGG ATC TTC CTG Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu 750 755 760	2547
ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG GAT GCT CGC CGG AAG Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys 765 770 775	2595
CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG TGG CGG AAG AAC CTG Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu 780 785 790	2643
CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC CCT AAA AAG AAA GCC Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Lys Ala 795 800 805 810	2691
ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC AGC TTC AAG AGG CGT Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg 815 820 825	2739
AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT CTT CAA CCC TGC CCT Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro 830 835 840	2787
GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG CCC CCG CCC TCG CTC Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Ser Leu 845 850 855	2835
CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA ACC AGC ACT CCC AGG Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg 860 865 870	2883

GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC GCT CTG CCC CTC CGT	2931
Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg	
875 880 885 890	
CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC ACC TCC CGG TGT ATG	2979
Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met	
895 900 905	
CAG TGG TGATGCCTAA AGGAATGTCA CG	3007
Gln Trp	

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 908 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser	
1 5 10 15	
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val	
20 25 30	
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln	
35 40 45	
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser	
50 55 60	
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu	
65 70 75 80	
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro	
85 90 95	
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly	
100 105 110	
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr	
115 120 125	
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr	
130 135 140	
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp	
145 150 155 160	
Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala	
165 170 175	
Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ala Glu	
180 185 190	
Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu	
195 200 205	
Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser	
210 215 220	
Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met	

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225	230	235	240
Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val			
245	250	255	
Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe			
260	265	270	
Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu			
275	280	285	
Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val			
290	295	300	
Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys			
305	310	315	320
Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His			
325	330	335	
Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys			
340	345	350	
Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys			
355	360	365	
Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro			
370	375	380	
Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg			
385	390	395	400
Thr Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe			
405	410	415	
Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly			
420	425	430	
Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro			
435	440	445	
Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro			
450	455	460	
Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg			
465	470	475	480
Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu			
485	490	495	
Leu Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu			
500	505	510	
Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu			
515	520	525	
Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly			
530	535	540	
Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser			
545	550	555	560
Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe Ala Met Ile Ile Val			
565	570	575	
Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro			
580	585	590	

Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser  
595 600 605

Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr  
610 615 620

Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys  
625 630 635 640

His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn  
645 650 655

Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala  
660 665 670

Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser  
675 680 685

Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val  
690 695 700

Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu  
705 710 715 720

Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala  
725 730 735

Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val  
740 745 750

Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala  
755 760 765

Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe  
770 775 780

Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly  
785 790 795 800

Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr  
805 810 815

Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr  
820 825 830

Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu  
835 840 845

Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro  
850 855 860

Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe  
865 870 875 880

Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala  
885 890 895

His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp  
900 905

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3998 base pairs  
(B) TYPE: nucleic acid

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- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 262..3093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CGCGCAGAG	240
CCAGGCCCCG GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC	627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr	
110 115 120	
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG	675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu	
125 130 135	
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG	723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met	
140 145 150	
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC	771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp	
155 160 165 170	
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG	819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu	

	175	180	185	
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG Arg Glu Ser Lys Ser Lys Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu	190	195	200	867
TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe	205	210	215	915
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu	220	225	230	963
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala	235	240	245	1011
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC TCC GGG TAC Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Ser Gly Tyr	255	260	265	1059
GTG TGG CTG GTC GGC GAG CGC GAG ATC TCG GGG AAC GCC CTG CGC TAC Val Trp Leu Val Gly Glu Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr	270	275	280	1107
GCC CCA GAC GGC ATC CTC GGG CTG CAG CTC ATC AAC GGC AAG AAC GAG Ala Pro Asp Gly Ile Leu Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu	285	290	295	1155
TCG GCC CAC ATC AGC GAC GCC GTG GGC GTG GTG GCC CAG GCC GTG CAC Ser Ala His Ile Ser Asp Ala Val Gly Val Val Ala Gln Ala Val His	300	305	310	1203
GAG CTC CTC GAG AAG GAG AAC ATC ACC GAC CCG CCG CGG GGC TGC GTG Glu Leu Leu Glu Lys Glu Asn Ile Thr Asp Pro Pro Arg Gly Cys Val	315	320	325	1251
GGC AAC ACC AAC ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu	335	340	345	1299
ATG TCT TCC AAG TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT Met Ser Ser Lys Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn	350	355	360	1347
GAG GAT GGG GAC CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln	365	370	375	1395
AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile	380	385	390	1443
CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro	395	400	405	1491
CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln	415	420	425	1539
GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys	430	435	440	1587
GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC				1635

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Glu	Glu	Phe	Thr	Val	Asn	Gly	Asp	Pro	Val	Lys	Lys	Val	Ile	Cys	Thr	
445					450					455						
GGG	CCC	AAC	GAC	ACG	TCG	CCG	GGC	AGC	CCC	CGC	CAC	ACG	GTG	CCT	CAG	1683
Gly	Pro	Asn	Asp	Thr	Ser	Pro	Gly	Ser	Pro	Arg	His	Thr	Val	Pro	Gln	
460				465						470						
TGT	TGC	TAC	GGC	TTT	TGC	ATC	GAC	CTG	CTC	ATC	AAG	CTG	GCA	CGG	ACC	1731
Cys	Cys	Tyr	Gly	Phe	Cys	Ile	Asp	Leu	Ile	Lys	Leu	Ala	Arg	Thr		
475				480					485				490			
ATG	AAC	TTC	ACC	TAC	GAG	GTG	CAC	CTG	GTG	GCA	GAT	GGC	AAG	TTC	GGC	1779
Met	Asn	Phe	Thr	Tyr	Glu	Val	His	Leu	Val	Ala	Asp	Gly	Lys	Phe	Gly	
495					500					505						
ACA	CAG	GAG	CGG	GTG	AAC	AAC	AGC	AAC	AAG	AAG	GAG	TGG	AAT	GGG	ATG	1827
Thr	Gln	Glu	Arg	Val	Asn	Asn	Ser	Asn	Lys	Lys	Glu	Trp	Asn	Gly	Met	
510						515						520				
ATG	GGC	GAG	CTG	CTC	AGC	GGG	CAG	GCA	GAC	ATG	ATC	GTG	GCG	CCG	CTA	1875
Met	Gly	Glu	Leu	Leu	Ser	Gly	Gln	Ala	Asp	Met	Ile	Val	Ala	Pro	Leu	
525						530					535					
ACC	ATA	AAC	AAC	GAG	CGC	GCG	CAG	TAC	ATC	GAG	TTT	TCC	AAG	CCC	TTC	1923
Thr	Ile	Asn	Asn	Glu	Arg	Ala	Gln	Tyr	Ile	Glu	Phe	Ser	Lys	Pro	Phe	
540						545				550						
AAG	TAC	CAG	GGC	CTG	ACT	ATT	CTG	GTC	AAG	AAG	GAG	ATT	CCC	CGG	AGC	1971
Lys	Tyr	Gln	Gly	Leu	Thr	Ile	Leu	Val	Lys	Lys	Glu	Ile	Pro	Arg	Ser	
555						560			565				570			
ACG	CTG	GAC	TCG	TTC	ATG	CAG	CCG	TTC	CAG	AGC	ACA	CTG	TGG	CTG	CTG	2019
Thr	Leu	Asp	Ser	Phe	Met	Gln	Pro	Phe	Gln	Ser	Thr	Leu	Trp	Leu	Leu	
575							580					585				
GTG	GGG	CTG	TCG	GTG	CAC	GTG	GTG	GCC	GTG	ATG	CTG	TAC	CTG	CTG	GAC	2067
Val	Gly	Leu	Ser	Val	His	Val	Ala	Val	Met	Leu	Tyr	Leu	Leu	Asp		
590							595					600				
CGC	TTC	AGC	CCC	TTC	GGC	CGG	TTC	AAG	GTG	AAC	AGC	GAG	GAG	GAG	GAG	2115
Arg	Phe	Ser	Pro	Phe	Gly	Arg	Phe	Lys	Val	Asn	Ser	Glu	Glu	Glu	Glu	
605							610					615				
GAG	GAC	GCA	CTG	ACC	CTG	TCC	TCG	GCC	ATG	TGG	TTC	TCC	TGG	GGC	GTC	2163
Glu	Asp	Ala	Leu	Thr	Leu	Ser	Ser	Ala	Met	Trp	Phe	Ser	Trp	Gly	Val	
620						625					630					
CTG	CTC	AAC	TCC	GGC	ATC	GGG	GAA	GGC	GCC	CCC	AGA	AGC	TTC	TCA	GCG	2211
Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	
635						640				645			650			
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259
Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	
655							660					665				
TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GAC	CGG	CCG	GAG			2307
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	
670							675					680				
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355
Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	
685							690					695				
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403
Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	
700							705					710				

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CGG CGC CAG GTG GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC Arg Arg Gln Val Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His 715 720 725 730	2451
AAC TAC GAG AGT GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys 735 740 745	2499
CTG CAT GCC TTC ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG Leu His Ala Phe Ile Trp Asp Ser Ala Val Leu Glu Phe Glu Ala Ser 750 755 760	2547
CAG AAG TGC GAC CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC Gln Lys Cys Asp Leu Val Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly 765 770 775	2595
TTC GGC ATA GGC ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC Phe Gly Ile Gly Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser 780 785 790	2643
CTG TCC ATC CTC AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC Leu Ser Ile Leu Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp 795 800 805 810	2691
AAG ACG TGG GTT CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro 815 820 825	2739
GCG ACC CTT ACT TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT Ala Thr Leu Thr Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala 830 835 840	2787
GGG GGC ATC GTG GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC Gly Gly Ile Val Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr 845 850 855	2835
AAG CGG CAC AAG GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC Lys Arg His Lys Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala 860 865 870	2883
GCC GTT AAC GTG TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA Ala Val Asn Val Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg 875 880 885 890	2931
GCA GAG CCT GAC CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC Ala Glu Pro Asp Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser 895 900 905	2979
ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CAG Thr Leu Ala Ser Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Gln 910 915 920	3027
TAC CAT CCC ACT GAT ATC ACG GGC CCG CTC AAC CTC TCA GAT CCC TCG Tyr His Pro Thr Asp Ile Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser 925 930 935	3075
GTC AGC ACC GTG GTG TGAGGCCCGG GGAGGCCGCC ACCTGCCAG TTAGCCGGC Val Ser Thr Val Val 940	3130
CAAGGACACT GATGGGTCCT GCTGCTCGGG AAGGCCTGAG GGAAGCCCAC CCGCCCCAGA	3190
GAAGTGCCTAC CCTGGGCCTC CCGTCCGTCC GCCCCCCCAC CCCGCTGCCT GGCGGGCAGC	3250
CCCTGCTGGA CCAAGGTGCG GACCGGAGCG GCTGAGGACG GGGCAGAGCT GAGTCGGCTG	3310
GGCAGGGCCG CAGGGCGCTC CGGCAGAGGC AGGCCCCCTGG GGTCTCTGAG CAGTGGGGAG	3370

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CGGGGGCTAA	CTGCCCCCAG	GCGGAGGGGC	TTGGAGCAGA	GACGGCAGCC	CCATCCTTCC	3430
CGCAGCACCA	GCCTGAGCCA	CAGTGGGCC	CATGGCCCCA	GCTGGCTGGG	TCGCCCCCTCC	3490
TCGGGCGCCT	CGCCTCCTCT	GCAGCCTGAG	CTCCACCCCTC	CCCTCTTCTT	CGGGCACCGC	3550
CCACCAAACA	CCCCGTCTGC	CCCTTGACGC	CACACGCCGG	GGCTGGCGCT	GCCCTCCCCC	3610
ACGGCCGTCC	CTGACTTCCC	AGCTGGCAGC	GCCTCCCGCC	GCCTCGGGCC	GCCTCCTCCA	3670
GAATCGAGAG	GGCTGAGCCC	CTCCTCTCCT	CGTCCGGCCT	GCAGCACAGA	AGGGGGCCTC	3730
CCCGGGGGTC	CCCGGACGCT	GGCTCGGGAC	TGTCTTCAAC	CCTGCCCTGC	ACCTTGGGCA	3790
CGGGAGAGCG	CCACCCGCC	GCCCCCGCCC	TCGCTCCGGG	TGCGTGACCG	GCCCGCCACC	3850
TTGTACAGAA	CCAGCACTCC	CAGGGCCCGA	GCGCGTGCCT	TCCCCGTGCG	CAGCCGCGCT	3910
CTGCCCCCTCC	GTCCCCAGGG	TGCAGGGCG	CACCGCCCCAA	CCCCCACCTC	CCGGTGTATG	3970
CAGTGGTGAT	GCCTAAAGGA	ATGTCACG				3998

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 943 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

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Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser
1 5 10 15

Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val
20 25 30

Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln
35 40 45

Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser
50 55 60

Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu
65 70 75 80

Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro
85 90 95

Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly
100 105 110

Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr
115 120 125

Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr
130 135 140

Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp
145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala
165 170 175

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Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys  
180 185 190

Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg  
195 200 205

Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn  
210 215 220

Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile  
225 230 235 240

Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala  
245 250 255

Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu  
260 265 270

Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu  
275 280 285

Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp  
290 295 300

Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu  
305 310 315 320

Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp  
325 330 335

Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala  
340 345 350

Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys  
355 360 365

Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln  
370 375 380

Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile  
385 390 395 400

Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser  
405 410 415

Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val  
420 425 430

Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn  
435 440 445

Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser  
450 455 460

Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys  
465 470 475 480

Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu  
485 490 495

Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn  
500 505 510

Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser  
515 520 525

Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg

530	535	540
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr		
545	550	555
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met		
565	570	575
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His		
580	585	590
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly		
595	600	605
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu		
610	615	620
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile		
625	630	635
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val		
645	650	655
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu		
660	665	670
Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile		
675	680	685
Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr		
690	695	700
Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu		
705	710	715
Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala		
725	730	735
Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp		
740	745	750
Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val		
755	760	765
Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg		
770	775	780
Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser		
785	790	795
His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr		
805	810	815
Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu		
820	825	830
Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly		
835	840	845
Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala		
850	855	860
Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg		
865	870	875
Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys		

885	890	895
Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe		
900	905	910
Lys Arg Arg Arg Ser Ser Lys Asp Thr Gln Tyr His Pro Thr Asp Ile		
915	920	925
Thr Gly Pro Leu Asn Leu Ser Asp Pro Ser Val Ser Thr Val Val		
930	935	940

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3274 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 262..3255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGCTG AGCGCCGAGC CCCCGCGCAC GCTTCAGCCC CCCTTCCCTC GGCCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCG GAAGCCCCGC GGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435
Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile	
45 50 55	
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG	483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met	
60 65 70	
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC	531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile	
75 80 85 90	
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT	579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro	
95 100 105	

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GTC	TCC	TAC	ACA	GCC	GGC	TTC	TAC	CGC	ATA	CCC	GTG	CTG	GGG	CTG	ACC	627
Val	Ser	Tyr	Thr	Ala	Gly	Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	
110								115				120				
ACC	CGC	ATG	TCC	ATC	TAC	TCG	GAC	AAG	AGC	ATC	CAC	CTG	AGC	TTC	CTG	675
Thr	Arg	Met	Ser	Ile	Tyr	Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	
125							130				135					
CGC	ACC	GTG	CCG	CCC	TAC	TCC	CAC	CAG	TCC	AGC	GTG	TGG	TTT	GAG	ATG	723
Arg	Thr	Val	Pro	Pro	Tyr	Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	
140					145					150						
ATG	CGT	GTC	TAC	AGC	TGG	AAC	CAC	ATC	ATC	CTG	CTG	GTC	AGC	GAC	GAC	771
Met	Arg	Val	Tyr	Ser	Trp	Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	
155					160				165			170				
CAC	GAG	GGC	CGG	GCG	GCT	CAG	AAA	CGC	CTG	GAG	ACG	CTG	CTG	GAG	GAG	819
His	Glu	Gly	Arg	Ala	Ala	Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	
175						180				185						
CGT	GAG	TCC	AAG	AGT	AAA	AAA	AGG	AAC	TAT	GAA	AAC	CTC	GAC	CAA	CTG	867
Arg	Glu	Ser	Lys	Ser	Lys	Lys	Arg	Asn	Tyr	Glu	Asn	Leu	Asp	Gln	Leu	
190					195					200						
TCC	TAT	GAC	AAC	AAG	CGC	GGA	CCC	AAG	GCA	GAG	AAG	GTG	CTG	CAG	TTT	915
Ser	Tyr	Asp	Asn	Lys	Arg	Gly	Pro	Lys	Ala	Glu	Lys	Val	Leu	Gln	Phe	
205					210				215							
GAC	CCA	GGG	ACC	AAG	AAC	GTG	ACG	GCC	CTG	CTG	ATG	GAG	GCG	AAA	GAG	963
Asp	Pro	Gly	Thr	Lys	Asn	Val	Thr	Ala	Leu	Leu	Met	Glu	Ala	Lys	Glu	
220					225				230							
CTG	GAG	GCC	CGG	GTC	ATC	ATC	CTT	TCT	GCC	AGC	GAG	GAC	GAT	GCT	GCC	1011
Leu	Glu	Ala	Arg	Val	Ile	Ile	Leu	Ser	Ala	Ser	Glu	Asp	Asp	Ala	Ala	
235					240				245			250				
ACT	GTA	TAC	CGC	GCA	GCC	GCG	ATG	CTG	AAC	ATG	ACG	GGC	TCC	GGG	TAC	1059
Thr	Val	Tyr	Arg	Ala	Ala	Ala	Met	Leu	Asn	Met	Thr	Gly	Ser	Gly	Tyr	
255						260				265						
GTG	TGG	CTG	GTC	GGC	GAG	CGC	GAG	ATC	TCG	GGG	AAC	GCC	CTG	CGC	TAC	1107
Val	Trp	Leu	Val	Gly	Glu	Arg	Glu	Ile	Ser	Gly	Asn	Ala	Leu	Arg	Tyr	
270					275				280							
GCC	CCA	GAC	GGC	ATC	CTC	GGG	CTG	CAG	CTC	ATC	AAC	GGC	AAG	AAC	GAG	1155
Ala	Pro	Asp	Gly	Ile	Leu	Gly	Leu	Gln	Leu	Ile	Asn	Gly	Lys	Asn	Glu	
285					290				295							
TCG	GCC	CAC	ATC	AGC	GAC	GCC	GTG	GGC	GTG	GTC	GCC	CAG	GCC	GTG	CAC	1203
Ser	Ala	His	Ile	Ser	Asp	Ala	Val	Gly	Val	Val	Ala	Gln	Ala	Val	His	
300					305				310							
GAG	CTC	CTC	GAG	AAG	GAG	AAC	ATC	ACC	GAC	CCG	CCG	CGG	GGC	TGC	GTG	1251
Glu	Leu	Leu	Glu	Lys	Glu	Asn	Ile	Thr	Asp	Pro	Pro	Arg	Gly	Cys	Val	
315					320				325			330				
GGC	AAC	ACC	AAC	ATC	TGG	AAG	ACC	GGG	CCG	CTC	TTC	AAG	AGA	GTG	CTG	1299
Gly	Asn	Thr	Asn	Ile	Trp	Lys	Thr	Gly	Pro	Leu	Phe	Lys	Arg	Val	Leu	
335						340				345						
ATG	TCT	TCC	AAG	TAT	GCG	GAT	GGG	GTG	ACT	GGT	CGC	GTG	GAG	TTC	AAT	1347
Met	Ser	Ser	Lys	Tyr	Ala	Asp	Gly	Val	Thr	Gly	Arg	Val	Glu	Phe	Asn	
350					355				360							
GAG	GAT	GGG	GAC	CGG	AAG	TTC	GCC	AAC	TAC	AGC	ATC	ATG	AAC	CTG	CAG	1395
Glu	Asp	Gly	Asp	Arg	Lys	Phe	Ala	Asn	Tyr	Ser	Ile	Met	Asn	Leu	Gln	

	365	370	375	
AAC CGC AAG CTG GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC Asn Arg Lys Leu Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile 380 385 390				1443
CCT AAT GAC AGG AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro 395 400 405 410				1491
CGA GGG TAC CAG ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln 415 420 425				1539
GAG CCC TTC GTG TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG Glu Pro Phe Val Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys 430 435 440				1587
GAG GAG TTC ACA GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC Glu Glu Phe Thr Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr 445 450 455				1635
GGG CCC AAC GAC ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln 460 465 470				1683
TGT TGC TAC GGC TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr 475 480 485 490				1731
ATG AAC TTC ACC TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC Met Asn Phe Thr Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly 495 500 505				1779
ACA CAG GAG CGG GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG Thr Gln Glu Arg Val Asn Asn Ser Asn Lys Lys Glu Trp Asn Gly Met 510 515 520				1827
ATG GGC GAG CTG CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA Met Gly Glu Leu Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu 525 530 535				1875
ACC ATA AAC AAC GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe 540 545 550				1923
AAG TAC CAG GGC CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CGG AGC Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser 555 560 565 570				1971
ACG CTG GAC TCG TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG Thr Leu Asp Ser Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu 575 580 585				2019
GTG GGG CTG TCG GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC Val Gly Leu Ser Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp 590 595 600				2067
CGC TTC AGC CCC TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG Arg Phe Ser Pro Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu 605 610 615				2115
GAG GAC GCA CTG ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC Glu Asp Ala Leu Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val 620 625 630				2163
CTG CTC AAC TCC GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG				2211

Leu	Leu	Asn	Ser	Gly	Ile	Gly	Glu	Gly	Ala	Pro	Arg	Ser	Phe	Ser	Ala	
635				640			645						650			
CGC	ATC	CTG	GGC	ATG	GTG	TGG	GCC	GGC	TTT	GCC	ATG	ATC	ATC	GTG	GCC	2259
Arg	Ile	Leu	Gly	Met	Val	Trp	Ala	Gly	Phe	Ala	Met	Ile	Ile	Val	Ala	
				655					660					665		
TCC	TAC	ACC	GCC	AAC	CTG	GCG	GCC	TTC	CTG	GTG	CTG	GAC	CGG	CCG	GAG	2307
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Leu	Val	Leu	Asp	Arg	Pro	Glu	
				670				675					680			
GAG	CGC	ATC	ACG	GGC	ATC	AAC	GAC	CCT	CGG	CTG	AGG	AAC	CCC	TCG	GAC	2355
Glu	Arg	Ile	Thr	Gly	Ile	Asn	Asp	Pro	Arg	Leu	Arg	Asn	Pro	Ser	Asp	
				685			690				695					
AAG	TTT	ATC	TAC	GCC	ACG	GTG	AAG	CAG	AGC	TCC	GTG	GAT	ATC	TAC	TTC	2403
Lys	Phe	Ile	Tyr	Ala	Thr	Val	Lys	Gln	Ser	Ser	Val	Asp	Ile	Tyr	Phe	
				700			705				710					
CGG	CGC	CAG	GTG	GAG	CTG	AGC	ACC	ATG	TAC	CGG	CAT	ATG	GAG	AAG	CAC	2451
Arg	Arg	Gln	Val	Glu	Leu	Ser	Thr	Met	Tyr	Arg	His	Met	Glu	Lys	His	
				715			720			725			730			
AAC	TAC	GAG	AGT	GCG	GCG	GAG	GCC	ATC	CAG	GCC	GTG	AGA	GAC	AAC	AAG	2499
Asn	Tyr	Glu	Ser	Ala	Ala	Glu	Ala	Ile	Gln	Ala	Val	Arg	Asp	Asn	Lys	
				735			740				745					
CTG	CAT	GCC	TTC	ATC	TGG	GAC	TCG	GCG	GTG	CTG	GAG	TTC	GAG	GCC	TCG	2547
Leu	His	Ala	Phe	Ile	Trp	Asp	Ser	Ala	Val	Leu	Glu	Phe	Glu	Ala	Ser	
				750			755				760					
CAG	AAG	TGC	GAC	CTG	G TG	ACG	ACT	GGA	GAG	CTG	TTT	TTC	CGC	TCG	G GC	2595
Gln	Lys	Cys	Asp	Leu	Val	Thr	Thr	Gly	Glu	Leu	Phe	Phe	Arg	Ser	Gly	
				765			770				775					
TTC	GGC	ATA	GGC	ATG	CGC	AAA	GAC	AGC	CCC	TGG	AAG	CAG	AAC	GTC	TCC	2643
Phe	Gly	Ile	Gly	Met	Arg	Lys	Asp	Ser	Pro	Trp	Lys	Gln	Asn	Val	Ser	
				780			785			790						
CTG	TCC	ATC	CTC	AAG	TCC	CAC	GAG	AAT	GGC	TTC	ATG	GAA	GAC	CTG	GAC	2691
Leu	Ser	Ile	Leu	Lys	Ser	His	Glu	Asn	Gly	Phe	Met	Glu	Asp	Leu	Asp	
				795			800			805			810			
AAG	ACG	TGG	GTT	CGG	TAT	CAG	GAA	TGT	GAC	TCG	CGC	AGC	AAC	GCC	CCT	2739
Lys	Thr	Trp	Val	Arg	Tyr	Gln	Glu	Cys	Asp	Ser	Arg	Ser	Asn	Ala	Pro	
				815			820				825					
GCG	ACC	CTT	ACT	TTT	GAG	AAC	ATG	GCC	GGG	GTC	TTC	ATG	CTG	GTA	GCT	2787
Ala	Thr	Leu	Thr	Phe	Glu	Asn	Met	Ala	Gly	Val	Phe	Met	Leu	Val	Ala	
				830			835				840					
GGG	GGC	ATC	GTG	GCC	GGG	ATC	TTC	CTG	ATT	TTC	ATC	GAG	ATT	GCC	TAC	2835
Gly	Gly	Ile	Val	Ala	Gly	Ile	Phe	Leu	Ile	Phe	Ile	Glu	Ile	Ala	Tyr	
				845			850				855					
AAG	CGG	CAC	AAG	GAT	GCT	CGC	CGG	AAG	CAG	ATG	CAG	CTG	GCC	TTT	GCC	2883
Lys	Arg	His	Lys	Asp	Ala	Arg	Arg	Lys	Gln	Met	Gln	Leu	Ala	Phe	Ala	
				860			865				870					
GCC	GTT	AAC	GTG	TGG	CGG	AAG	AAC	CTG	CAG	GAT	AGA	AAG	AGT	GGT	AGA	2931
Ala	Val	Asn	Val	Trp	Arg	Lys	Asn	Leu	Gln	Asp	Arg	Lys	Ser	Gly	Arg	
				875			880			885			890			
GCA	GAG	CCT	GAC	CCT	AAA	AAG	AAA	GCC	ACA	TTT	AGG	GCT	ATC	ACC	TCC	2979
Ala	Glu	Pro	Asp	Pro	Lys	Lys	Lys	Ala	Thr	Phe	Arg	Ala	Ile	Thr	Ser	
				895			900				905					

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ACC CTG GCT TCC AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu 910 915 920	3027
GCT CGG GAC TGT CTT CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser 925 930 935	3075
GCC ACC CGC CCG CCC CCG TCG CTC CGG GTG CGT GAC CGG CCC GCC Ala Thr Arg Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala 940 945 950	3123
ACC TTG TAC AGA ACC AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro 955 960 965 970	3171
GTG CGC AGC CGC GCT CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC Val Arg Ser Arg Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His 975 980 985	3219
CGC CCA ACC CCC ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA Arg Pro Thr Pro Thr Ser Arg Cys Met Gln Trp 990 995	3272
CG	3274

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 997 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Ser Thr Met Arg Leu Leu Thr Leu Ala Leu Leu Phe Ser Cys Ser 1 5 10 15
Val Ala Arg Ala Ala Cys Asp Pro Lys Ile Val Asn Ile Gly Ala Val 20 25 30
Leu Ser Thr Arg Lys His Glu Gln Met Phe Arg Glu Ala Val Asn Gln 35 40 45
Ala Asn Lys Arg His Gly Ser Trp Lys Ile Gln Leu Asn Ala Thr Ser 50 55 60
Val Thr His Lys Pro Asn Ala Ile Gln Met Ala Leu Ser Val Cys Glu 65 70 75 80
Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile Leu Val Ser His Pro Pro 85 90 95
Thr Pro Asn Asp His Phe Thr Pro Thr Pro Val Ser Tyr Thr Ala Gly 100 105 110
Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr Thr Arg Met Ser Ile Tyr 115 120 125
Ser Asp Lys Ser Ile His Leu Ser Phe Leu Arg Thr Val Pro Pro Tyr 130 135 140
Ser His Gln Ser Ser Val Trp Phe Glu Met Met Arg Val Tyr Ser Trp 145 150 155 160

Asn His Ile Ile Leu Leu Val Ser Asp Asp His Glu Gly Arg Ala Ala  
165 170 175

Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu Arg Glu Ser Lys Ser Lys  
180 185 190

Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg  
195 200 205

Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn  
210 215 220

Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile  
225 230 235 240

Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala  
245 250 255

Ala Met Leu Asn Met Thr Gly Ser Gly Tyr Val Trp Leu Val Gly Glu  
260 265 270

Arg Glu Ile Ser Gly Asn Ala Leu Arg Tyr Ala Pro Asp Gly Ile Leu  
275 280 285

Gly Leu Gln Leu Ile Asn Gly Lys Asn Glu Ser Ala His Ile Ser Asp  
290 295 300

Ala Val Gly Val Val Ala Gln Ala Val His Glu Leu Leu Glu Lys Glu  
305 310 315 320

Asn Ile Thr Asp Pro Pro Arg Gly Cys Val Gly Asn Thr Asn Ile Trp  
325 330 335

Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala  
340 345 350

Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys  
355 360 365

Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln  
370 375 380

Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile  
385 390 395 400

Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser  
405 410 415

Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val  
420 425 430

Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn  
435 440 445

Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser  
450 455 460

Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys  
465 470 475 480

Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu  
485 490 495

Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn  
500 505 510

Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser

515	520	525
Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg		
530	535	540
Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr		
545	550	555
560		
Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met		
565	570	575
Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His		
580	585	590
Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly		
595	600	605
Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu		
610	615	620
Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile		
625	630	635
640		
Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val		
645	650	655
Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu		
660	665	670
Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile		
675	680	685
Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr		
690	695	700
Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu		
705	710	715
720		
Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala		
725	730	735
Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp		
740	745	750
Asp Ser Ala Val Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val		
755	760	765
Thr Thr Gly Glu Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg		
770	775	780
Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser		
785	790	795
800		
His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr		
805	810	815
Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu		
820	825	830
Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly		
835	840	845
Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala		
850	855	860
Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg		

865	870	875	880
Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys			
885	890	895	
Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe			
900	905	910	
Lys Arg Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln			
915	920	925	
Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro			
930	935	940	
Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser			
945	950	955	960
Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu			
965	970	975	
Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser			
980	985	990	
Arg Cys Met Gln Trp			
995			

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3070 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 262..3051

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CAAGCCGGGC GTTCGGAGCT GTGCCCGGCC CCGCTTCAGC ACCGCGGACA GCGCCGGCCG	60
CGTGGGGCTG AGCGCCGAGC CCCC CGCGCAC GCTTCAGCCC CCCTTCCCTC GGCGACGTC	120
CCGGGACCGC CGCTCCGGGG GAGACGTGGC GTCCGCAGCC CGCGGGGCCG GGCGAGCGCA	180
GGACGGCCCCG GAAGCCCCGC GGGGGATGCG CCGAGGGCCC CGCGTTCGCG CCGCGCAGAG	240
CCAGGCCCGC GGCCCGAGCC C ATG AGC ACC ATG CGC CTG CTG ACG CTC GCC	291
Met Ser Thr Met Arg Leu Leu Thr Leu Ala	
1 5 10	
CTG CTG TTC TCC TGC TCC GTC GCC CGT GCC GCG TGC GAC CCC AAG ATC	339
Leu Leu Phe Ser Cys Ser Val Ala Arg Ala Ala Cys Asp Pro Lys Ile	
15 20 25	
GTC AAC ATT GGC GCG GTG CTG AGC ACG CGG AAG CAC GAG CAG ATG TTC	387
Val Asn Ile Gly Ala Val Leu Ser Thr Arg Lys His Glu Gln Met Phe	
30 35 40	
CGC GAG GCC GTG AAC CAG GCC AAC AAG CGG CAC GGC TCC TGG AAG ATT	435

Arg Glu Ala Val Asn Gln Ala Asn Lys Arg His Gly Ser Trp Lys Ile		
45 50 55		
CAG CTC AAT GCC ACC TCC GTC ACG CAC AAG CCC AAC GCC ATC CAG ATG		483
Gln Leu Asn Ala Thr Ser Val Thr His Lys Pro Asn Ala Ile Gln Met		
60 65 70		
GCT CTG TCG GTG TGC GAG GAC CTC ATC TCC AGC CAG GTC TAC GCC ATC		531
Ala Leu Ser Val Cys Glu Asp Leu Ile Ser Ser Gln Val Tyr Ala Ile		
75 80 85 90		
CTA GTT AGC CAT CCA CCT ACC CCC AAC GAC CAC TTC ACT CCC ACC CCT		579
Leu Val Ser His Pro Pro Thr Pro Asn Asp His Phe Thr Pro Thr Pro		
95 100 105		
GTC TCC TAC ACA GCC GGC TTC TAC CGC ATA CCC GTG CTG GGG CTG ACC		627
Val Ser Tyr Thr Ala Gly Phe Tyr Arg Ile Pro Val Leu Gly Leu Thr		
110 115 120		
ACC CGC ATG TCC ATC TAC TCG GAC AAG AGC ATC CAC CTG AGC TTC CTG		675
Thr Arg Met Ser Ile Tyr Ser Asp Lys Ser Ile His Leu Ser Phe Leu		
125 130 135		
CGC ACC GTG CCG CCC TAC TCC CAC CAG TCC AGC GTG TGG TTT GAG ATG		723
Arg Thr Val Pro Pro Tyr Ser His Gln Ser Ser Val Trp Phe Glu Met		
140 145 150		
ATG CGT GTC TAC AGC TGG AAC CAC ATC ATC CTG CTG GTC AGC GAC GAC		771
Met Arg Val Tyr Ser Trp Asn His Ile Ile Leu Leu Val Ser Asp Asp		
155 160 165 170		
CAC GAG GGC CGG GCG GCT CAG AAA CGC CTG GAG ACG CTG CTG GAG GAG		819
His Glu Gly Arg Ala Ala Gln Lys Arg Leu Glu Thr Leu Leu Glu Glu		
175 180 185		
CGT GAG TCC AAG AGT AAA AAA AGG AAC TAT GAA AAC CTC GAC CAA CTG		867
Arg Glu Ser Lys Ser Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu		
190 195 200		
TCC TAT GAC AAC AAG CGC GGA CCC AAG GCA GAG AAG GTG CTG CAG TTT		915
Ser Tyr Asp Asn Lys Arg Gly Pro Lys Ala Glu Lys Val Leu Gln Phe		
205 210 215		
GAC CCA GGG ACC AAG AAC GTG ACG GCC CTG CTG ATG GAG GCG AAA GAG		963
Asp Pro Gly Thr Lys Asn Val Thr Ala Leu Leu Met Glu Ala Lys Glu		
220 225 230		
CTG GAG GCC CGG GTC ATC ATC CTT TCT GCC AGC GAG GAC GAT GCT GCC		1011
Leu Glu Ala Arg Val Ile Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala		
235 240 245 250		
ACT GTA TAC CGC GCA GCC GCG ATG CTG AAC ATG ACG GGC AAC ACC AAC		1059
Thr Val Tyr Arg Ala Ala Ala Met Leu Asn Met Thr Gly Asn Thr Asn		
255 260 265		
ATC TGG AAG ACC GGG CCG CTC TTC AAG AGA GTG CTG ATG TCT TCC AAG		1107
Ile Trp Lys Thr Gly Pro Leu Phe Lys Arg Val Leu Met Ser Ser Lys		
270 275 280		
TAT GCG GAT GGG GTG ACT GGT CGC GTG GAG TTC AAT GAG GAT GGG GAC		1155
Tyr Ala Asp Gly Val Thr Gly Arg Val Glu Phe Asn Glu Asp Gly Asp		
285 290 295		
CGG AAG TTC GCC AAC TAC AGC ATC ATG AAC CTG CAG AAC CGC AAG CTG		1203
Arg Lys Phe Ala Asn Tyr Ser Ile Met Asn Leu Gln Asn Arg Lys Leu		
300 305 310		

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GTG CAA GTG GGC ATC TAC AAT GGC ACC CAC GTC ATC CCT AAT GAC AGG Val Gln Val Gly Ile Tyr Asn Gly Thr His Val Ile Pro Asn Asp Arg 315 320 325 330	1251
AAG ATC ATC TGG CCA GGC GGA GAG ACA GAG AAG CCT CGA GGG TAC CAG Lys Ile Ile Trp Pro Gly Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln 335 340 345	1299
ATG TCC ACC AGA CTG AAG ATT GTG ACG ATC CAC CAG GAG CCC TTC GTG Met Ser Thr Arg Leu Lys Ile Val Thr Ile His Gln Glu Pro Phe Val 350 355 360	1347
TAC GTC AAG CCC ACG CTG AGT GAT GGG ACA TGC AAG GAG GAG TTC ACA Tyr Val Lys Pro Thr Leu Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr 365 370 375	1395
GTC AAC GGC GAC CCA GTC AAG AAG GTG ATC TGC ACC GGG CCC AAC GAC Val Asn Gly Asp Pro Val Lys Lys Val Ile Cys Thr Gly Pro Asn Asp 380 385 390	1443
ACG TCG CCG GGC AGC CCC CGC CAC ACG GTG CCT CAG TGT TGC TAC GGC Thr Ser Pro Gly Ser Pro Arg His Thr Val Pro Gln Cys Cys Tyr Gly 395 400 405 410	1491
TTT TGC ATC GAC CTG CTC ATC AAG CTG GCA CGG ACC ATG AAC TTC ACC Phe Cys Ile Asp Leu Leu Ile Lys Leu Ala Arg Thr Met Asn Phe Thr 415 420 425	1539
TAC GAG GTG CAC CTG GTG GCA GAT GGC AAG TTC GGC ACA CAG GAG CGG Tyr Glu Val His Leu Val Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg 430 435 440	1587
GTG AAC AAC AGC AAC AAG AAG GAG TGG AAT GGG ATG ATG GGC GAG CTG Val Asn Ser Asn Lys Lys Glu Trp Asn Gly Met Met Gly Glu Leu 445 450 455	1635
CTC AGC GGG CAG GCA GAC ATG ATC GTG GCG CCG CTA ACC ATA AAC AAC Leu Ser Gly Gln Ala Asp Met Ile Val Ala Pro Leu Thr Ile Asn Asn 460 465 470	1683
GAG CGC GCG CAG TAC ATC GAG TTT TCC AAG CCC TTC AAG TAC CAG GGC Glu Arg Ala Gln Tyr Ile Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly 475 480 485 490	1731
CTG ACT ATT CTG GTC AAG AAG GAG ATT CCC CCG AGC ACG CTG GAC TCG Leu Thr Ile Leu Val Lys Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser 495 500 505	1779
TTC ATG CAG CCG TTC CAG AGC ACA CTG TGG CTG CTG GTG GGG CTG TCG Phe Met Gln Pro Phe Gln Ser Thr Leu Trp Leu Leu Val Gly Leu Ser 510 515 520	1827
GTG CAC GTG GTG GCC GTG ATG CTG TAC CTG CTG GAC CGC TTC AGC CCC Val His Val Val Ala Val Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro 525 530 535	1875
TTC GGC CGG TTC AAG GTG AAC AGC GAG GAG GAG GAG GAC GCA CTG Phe Gly Arg Phe Lys Val Asn Ser Glu Glu Glu Glu Asp Ala Leu 540 545 550	1923
ACC CTG TCC TCG GCC ATG TGG TTC TCC TGG GGC GTC CTG CTC AAC TCC Thr Leu Ser Ser Ala Met Trp Phe Ser Trp Gly Val Leu Leu Asn Ser 555 560 565 570	1971
GGC ATC GGG GAA GGC GCC CCC AGA AGC TTC TCA GCG CGC ATC CTG GGC Gly Ile Gly Glu Gly Ala Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly 575 580 585	2019

ATG GTG TGG GCC GGC TTT GCC ATG ATC ATC GTG GCC TCC TAC ACC GCC Met Val Trp Ala Gly Phe Ala Met Ile Ile Val Ala Ser Tyr Thr Ala 590 595 600	2067
AAC CTG GCG GCC TTC CTG GTG CTG GAC CGG CCG GAG GAG CGC ATC ACG Asn Leu Ala Ala Phe Leu Val Leu Asp Arg Pro Glu Glu Arg Ile Thr 605 610 615	2115
GGC ATC AAC GAC CCT CGG CTG AGG AAC CCC TCG GAC AAG TTT ATC TAC Gly Ile Asn Asp Pro Arg Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr 620 625 630	2163
GCC ACG GTG AAG CAG AGC TCC GTG GAT ATC TAC TTC CGG CGC CAG GTG Ala Thr Val Lys Gln Ser Ser Val Asp Ile Tyr Phe Arg Arg Gln Val 635 640 645 650	2211
GAG CTG AGC ACC ATG TAC CGG CAT ATG GAG AAG CAC AAC TAC GAG AGT Glu Leu Ser Thr Met Tyr Arg His Met Glu Lys His Asn Tyr Glu Ser 655 660 665	2259
GCG GCG GAG GCC ATC CAG GCC GTG AGA GAC AAC AAG CTG CAT GCC TTC Ala Ala Glu Ala Ile Gln Ala Val Arg Asp Asn Lys Leu His Ala Phe 670 675 680	2307
ATC TGG GAC TCG GCG GTG CTG GAG TTC GAG GCC TCG CAG AAG TGC GAC Ile Trp Asp Ser Ala Val Leu Glu Phe Ala Ser Gln Lys Cys Asp 685 690 695	2355
CTG GTG ACG ACT GGA GAG CTG TTT TTC CGC TCG GGC TTC GGC ATA GGC Leu Val Thr Thr Gly Glu Leu Phe Arg Ser Gly Phe Gly Ile Gly 700 705 710	2403
ATG CGC AAA GAC AGC CCC TGG AAG CAG AAC GTC TCC CTG TCC ATC CTC Met Arg Lys Asp Ser Pro Trp Lys Gln Asn Val Ser Leu Ser Ile Leu 715 720 725 730	2451
AAG TCC CAC GAG AAT GGC TTC ATG GAA GAC CTG GAC AAG ACG TGG GTT Lys Ser His Glu Asn Gly Phe Met Glu Asp Leu Asp Lys Thr Trp Val 735 740 745	2499
CGG TAT CAG GAA TGT GAC TCG CGC AGC AAC GCC CCT GCG ACC CTT ACT Arg Tyr Gln Glu Cys Asp Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr 750 755 760	2547
TTT GAG AAC ATG GCC GGG GTC TTC ATG CTG GTA GCT GGG GGC ATC GTG Phe Glu Asn Met Ala Gly Val Phe Met Leu Val Ala Gly Gly Ile Val 765 770 775	2595
GCC GGG ATC TTC CTG ATT TTC ATC GAG ATT GCC TAC AAG CGG CAC AAG Ala Gly Ile Phe Leu Ile Phe Ile Glu Ile Ala Tyr Lys Arg His Lys 780 785 790	2643
GAT GCT CGC CGG AAG CAG ATG CAG CTG GCC TTT GCC GCC GTT AAC GTG Asp Ala Arg Arg Lys Gln Met Gln Leu Ala Phe Ala Ala Val Asn Val 795 800 805 810	2691
TGG CGG AAG AAC CTG CAG GAT AGA AAG AGT GGT AGA GCA GAG CCT GAC Trp Arg Lys Asn Leu Gln Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp 815 820 825	2739
CCT AAA AAG AAA GCC ACA TTT AGG GCT ATC ACC TCC ACC CTG GCT TCC Pro Lys Lys Ala Thr Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser 830 835 840	2787
AGC TTC AAG AGG CGT AGG TCC TCC AAA GAC ACG CTG GCT CGG GAC TGT Ser Phe Lys Arg Arg Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys 845 850 855	2835

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CTT CAA CCC TGC CCT GCA CCT TGG GCA CGG GAG AGC GCC ACC CGC CCG	2883
Leu Gln Pro Cys Pro Ala Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro	
860 865 870	
CCC CCG CCC TCG CTC CGG GTG CGT GAC CGG CCC GCC ACC TTG TAC AGA	2931
Pro Pro Pro Ser Leu Arg Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg	
875 880 885 890	
ACC AGC ACT CCC AGG GCC CGA GCG CGT GCC TTC CCC GTG CGC AGC CGC	2979
Thr Ser Thr Pro Arg Ala Arg Ala Arg Ala Phe Pro Val Arg Ser Arg	
895 900 905	
GCT CTG CCC CTC CGT CCC CAG GGT GCA GGC GCG CAC CGC CCA ACC CCC	3027
Ala Leu Pro Leu Arg Pro Gln Gly Ala Gly Ala His Arg Pro Thr Pro	
910 915 920	
ACC TCC CGG TGT ATG CAG TGG TGATGCCTAA AGGAATGTCA CG	3070
Thr Ser Arg Cys Met Gln Trp	
925 930	

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 929 amino acids
    - (B) TYPE: amino acid
    - (D) TOPOLOGY: linear
  - ii) MOLECULE TYPE: protein
  - xii) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Ser	Thr	Met	Arg	Leu	Leu	Thr	Leu	Ala	Leu	Leu	Phe	Ser	Cys	Ser
1				5					10					15	
Val	Ala	Arg	Ala	Ala	Cys	Asp	Pro	Lys	Ile	Val	Asn	Ile	Gly	Ala	Val
				20				25					30		
Leu	Ser	Thr	Arg	Lys	His	Glu	Gln	Met	Phe	Arg	Glu	Ala	Val	Asn	Gln
				35			40					45			
Ala	Asn	Lys	Arg	His	Gly	Ser	Trp	Lys	Ile	Gln	Leu	Asn	Ala	Thr	Ser
				50			55				60				
Val	Thr	His	Lys	Pro	Asn	Ala	Ile	Gln	Met	Ala	Leu	Ser	Val	Cys	Glu
				65			70				75			80	
Asp	Leu	Ile	Ser	Ser	Gln	Val	Tyr	Ala	Ile	Leu	Val	Ser	His	Pro	Pro
				85					90				95		
Thr	Pro	Asn	Asp	His	Phe	Thr	Pro	Thr	Pro	Val	Ser	Tyr	Thr	Ala	Gly
				100				105					110		
Phe	Tyr	Arg	Ile	Pro	Val	Leu	Gly	Leu	Thr	Thr	Arg	Met	Ser	Ile	Tyr
				115				120				125			
Ser	Asp	Lys	Ser	Ile	His	Leu	Ser	Phe	Leu	Arg	Thr	Val	Pro	Pro	Tyr
				130			135				140				
Ser	His	Gln	Ser	Ser	Val	Trp	Phe	Glu	Met	Met	Arg	Val	Tyr	Ser	Trp
				145			150				155			160	
Asn	His	Ile	Ile	Leu	Leu	Val	Ser	Asp	Asp	His	Glu	Gly	Arg	Ala	Ala
				165				170				175			
Gln	Lys	Arg	Leu	Glu	Thr	Leu	Leu	Glu	Glu	Arg	Glu	Ser	Lys	Ser	Lys
				180				185				190			

Lys Arg Asn Tyr Glu Asn Leu Asp Gln Leu Ser Tyr Asp Asn Lys Arg  
195 200 205

Gly Pro Lys Ala Glu Lys Val Leu Gln Phe Asp Pro Gly Thr Lys Asn  
210 215 220

Val Thr Ala Leu Leu Met Glu Ala Lys Glu Leu Glu Ala Arg Val Ile  
225 230 235 240

Ile Leu Ser Ala Ser Glu Asp Asp Ala Ala Thr Val Tyr Arg Ala Ala  
245 250 255

Ala Met Leu Asn Met Thr Gly Asn Thr Asn Ile Trp Lys Thr Gly Pro  
260 265 270

Leu Phe Lys Arg Val Leu Met Ser Ser Lys Tyr Ala Asp Gly Val Thr  
275 280 285

Gly Arg Val Glu Phe Asn Glu Asp Gly Asp Arg Lys Phe Ala Asn Tyr  
290 295 300

Ser Ile Met Asn Leu Gln Asn Arg Lys Leu Val Gln Val Gly Ile Tyr  
305 310 315 320

Asn Gly Thr His Val Ile Pro Asn Asp Arg Lys Ile Ile Trp Pro Gly  
325 330 335

Gly Glu Thr Glu Lys Pro Arg Gly Tyr Gln Met Ser Thr Arg Leu Lys  
340 345 350

Ile Val Thr Ile His Gln Glu Pro Phe Val Tyr Val Lys Pro Thr Leu  
355 360 365

Ser Asp Gly Thr Cys Lys Glu Glu Phe Thr Val Asn Gly Asp Pro Val  
370 375 380

Lys Lys Val Ile Cys Thr Gly Pro Asn Asp Thr Ser Pro Gly Ser Pro  
385 390 395 400

Arg His Thr Val Pro Gln Cys Cys Tyr Gly Phe Cys Ile Asp Leu Leu  
405 410 415

Ile Lys Leu Ala Arg Thr Met Asn Phe Thr Tyr Glu Val His Leu Val  
420 425 430

Ala Asp Gly Lys Phe Gly Thr Gln Glu Arg Val Asn Asn Ser Asn Lys  
435 440 445

Lys Glu Trp Asn Gly Met Met Gly Glu Leu Leu Ser Gly Gln Ala Asp  
450 455 460

Met Ile Val Ala Pro Leu Thr Ile Asn Asn Glu Arg Ala Gln Tyr Ile  
465 470 475 480

Glu Phe Ser Lys Pro Phe Lys Tyr Gln Gly Leu Thr Ile Leu Val Lys  
485 490 495

Lys Glu Ile Pro Arg Ser Thr Leu Asp Ser Phe Met Gln Pro Phe Gln  
500 505 510

Ser Thr Leu Trp Leu Leu Val Gly Leu Ser Val His Val Val Ala Val  
515 520 525

Met Leu Tyr Leu Leu Asp Arg Phe Ser Pro Phe Gly Arg Phe Lys Val  
530 535 540

Asn Ser Glu Glu Glu Glu Asp Ala Leu Thr Leu Ser Ser Ala Met

545                550                555                560  
Trp Phe Ser Trp Gly Val Leu Leu Asn Ser Gly Ile Gly Glu Gly Ala  
565                570                575  
Pro Arg Ser Phe Ser Ala Arg Ile Leu Gly Met Val Trp Ala Gly Phe  
580                585                590  
Ala Met Ile Ile Val Ala Ser Tyr Thr Ala Asn Leu Ala Ala Phe Leu  
595                600                605  
  
Val Leu Asp Arg Pro Glu Glu Arg Ile Thr Gly Ile Asn Asp Pro Arg  
610                615                620  
Leu Arg Asn Pro Ser Asp Lys Phe Ile Tyr Ala Thr Val Lys Gln Ser  
625                630                635                640  
Ser Val Asp Ile Tyr Phe Arg Arg Gln Val Glu Leu Ser Thr Met Tyr  
645                650                655  
Arg His Met Glu Lys His Asn Tyr Glu Ser Ala Ala Glu Ala Ile Gln  
660                665                670  
Ala Val Arg Asp Asn Lys Leu His Ala Phe Ile Trp Asp Ser Ala Val  
675                680                685  
Leu Glu Phe Glu Ala Ser Gln Lys Cys Asp Leu Val Thr Thr Gly Glu  
690                695                700  
Leu Phe Phe Arg Ser Gly Phe Gly Ile Gly Met Arg Lys Asp Ser Pro  
705                710                715                720  
Trp Lys Gln Asn Val Ser Leu Ser Ile Leu Lys Ser His Glu Asn Gly  
725                730                735  
Phe Met Glu Asp Leu Asp Lys Thr Trp Val Arg Tyr Gln Glu Cys Asp  
740                745                750  
Ser Arg Ser Asn Ala Pro Ala Thr Leu Thr Phe Glu Asn Met Ala Gly  
755                760                765  
Val Phe Met Leu Val Ala Gly Gly Ile Val Ala Gly Ile Phe Leu Ile  
770                775                780  
Phe Ile Glu Ile Ala Tyr Lys Arg His Lys Asp Ala Arg Arg Lys Gln  
785                790                795                800  
Met Gln Leu Ala Phe Ala Ala Val Asn Val Trp Arg Lys Asn Leu Gln  
805                810                815  
Asp Arg Lys Ser Gly Arg Ala Glu Pro Asp Pro Lys Lys Ala Thr  
820                825                830  
Phe Arg Ala Ile Thr Ser Thr Leu Ala Ser Ser Phe Lys Arg Arg Arg  
835                840                845  
Ser Ser Lys Asp Thr Leu Ala Arg Asp Cys Leu Gln Pro Cys Pro Ala  
850                855                860  
Pro Trp Ala Arg Glu Ser Ala Thr Arg Pro Pro Pro Pro Ser Leu Arg  
865                870                875                880  
Val Arg Asp Arg Pro Ala Thr Leu Tyr Arg Thr Ser Thr Pro Arg Ala  
885                890                895  
Arg Ala Arg Ala Phe Pro Val Arg Ser Arg Ala Leu Pro Leu Arg Pro

900

905

910

Gln Gly Ala Gly Ala His Arg Pro Thr Pro Thr Ser Arg Cys Met Gln  
915 920 925

Trp

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..2324

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CC GGC CAC GTG TGG CTG GTG CCC AAC CTG GCG CTG GGC AGC ACC GAT Gly His Val Trp Leu Val Pro Asn Leu Ala Leu Gly Ser Thr Asp 1 5 10 15	47
GCG CCC CCC GCC ACC TTC CCC GTG GGC CTC ATC AGC GTC GTC ACC GAG Ala Pro Pro Ala Thr Phe Pro Val Gly Leu Ile Ser Val Val Thr Glu 20 25 30	95
AGC TGG CGC CTC AGC CTG CGC CAG AAG GTG CGC GAC GGC GTG GCC ATT Ser Trp Arg Leu Ser Leu Arg Gln Lys Val Arg Asp Gly Val Ala Ile 35 40 45	143
CTG GCC CTG GGC GCC CAC AGC TAC TGG CGC CAG CAT GGA ACC CTG CCA Leu Ala Leu Gly Ala His Ser Tyr Trp Arg Gln His Gly Thr Leu Pro 50 55 60	191
GCC CCG GCC GGG GAC TGC CGT GTT CAC CCT GGG CCC GTC AGC CCT GCC Ala Pro Ala Gly Asp Cys Arg Val His Pro Gly Pro Val Ser Pro Ala 65 70 75	239
CGG GAG GCC TTC TAC AGG CAC CTA CTG AAT GTC ACC TGG GAG GGC CGA Arg Glu Ala Phe Tyr Arg His Leu Leu Asn Val Thr Trp Glu Gly Arg 80 85 90 95	287
GAC TTC TCC TTC AGC CCT GGT GGG TAC CTG GTC CAG CCC ACC ATG GTG Asp Phe Ser Phe Gly Gly Tyr Leu Val Gln Pro Thr Met Val 100 105 110	335
GTG ATC GCC CTC AAC CGG CAC CGC CTC TGG GAG ATG GTG GGG CGC TGG Val Ile Ala Leu Asn Arg His Arg Leu Trp Glu Met Val Gly Arg Trp 115 120 125	383
GAG CAT GGC GTC CTA TAC ATG AAG TAC CCC GTG TGG CCT CGC TAC AGT Glu His Gly Val Leu Tyr Met Lys Tyr Pro Val Trp Pro Arg Tyr Ser 130 135 140	431
GCC TCT CTG CAG CCT GTG GTG GAC AGT CGG CAC CTG ACG GTG GCC ACG Ala Ser Leu Gln Pro Val Val Asp Ser Arg His Leu Thr Val Ala Thr 145 150 155	479

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CTG GAA GAG CGG CCC TTT GTC ATC GTG GAG AGC CCT GAC CCT GGC ACA Leu Glu Glu Arg Pro Phe Val Ile Val Glu Ser Pro Asp Pro Gly Thr 160 165 170 175	527
GGA GGC TGT GTC CCC AAC ACC GTG CCC TGC CGC AGG CAG AGC AAC CAC Gly Gly Cys Val Pro Asn Thr Val Pro Cys Arg Arg Gln Ser Asn His 180 185 190	575
ACC TTC AGC AGC GGG GAC GTG GCC CCC TAC ACC AAG CTC TGC TGT AAG Thr Phe Ser Ser Gly Asp Val Ala Pro Tyr Thr Lys Leu Cys Cys Lys 195 200 205	623
GGA TTC TGC ATC GAC ATC CTC AAG AAG CTG GCC AGA GTG GTC AAA TTC Gly Phe Cys Ile Asp Ile Leu Lys Lys Leu Ala Arg Val Val Lys Phe 210 215 220	671
TCC TAC GAC CTG TAC CTG GTG ACC AAC GGC AAG CAT GGC AAG CGG GTG Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys Arg Val 225 230 235	719
CGC GGC GTA TGG AAC GGC ATG ATT GGG GAG GTG TAC TAC AAG CGG GCA Arg Gly Val Trp Asn Gly Met Ile Gly Glu Val Tyr Tyr Lys Arg Ala 240 245 250 255	767
GAC ATG GCC ATC GGC TCC CTC ACC ATC AAT GAG GAA CGC TCC GAG ATC Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Ile 260 265 270	815
GTA GAC TTC TCT GTA CCC TTT GTG GAG ACG GGC ATC AGT GTG ATG GTG Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val 275 280 285	863
GCT CGC AGC AAT GGC ACC GTC TCC CCC TCG GCC TTC TTG GAG CCA TAT Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Tyr 290 295 300	911
AGC CCT GCA GTG TGG GTG ATG ATG TTT GTC ATG TGC CTC ACT GTG GTG Ser Pro Ala Val Trp Val Met Met Phe Val Met Cys Leu Thr Val Val 305 310 315	959
GCC ATC ACC GTC TTC ATG TTC GAG TAC TTC AGC CCT GTC AGC TAC AAC Ala Ile Thr Val Phe Met Phe Glu Tyr Phe Ser Pro Val Ser Tyr Asn 320 325 330 335	1007
CAG AAC CTC ACC AGA GGC AAG AAG TCC GGG GGC CCA GCT TTC ACT ATC Gln Asn Leu Thr Arg Gly Lys Lys Ser Gly Gly Pro Ala Phe Thr Ile 340 345 350	1055
GGC AAG TCC GTG TGG CTG CTG TGG GCG CTG GTC TTC AAC AAC TCA GTG Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn Ser Val 355 360 365	1103
CCC ATC GAG AAC CCG CGG GGC ACC ACC AGC AAG ATC ATG GTT CTG GTC Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val Leu Val 370 375 380	1151
TGG GCC TTC TTT GCT GTC ATC TTC CTC GCC AGA TAC ACG GCC AAC CTG Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala Asn Leu 385 390 395	1199
GCC GCC TTC ATG ATC CAA GAG CAA TAC ATC GAC ACT GTG TCG GGC CTC Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser Gly Leu 400 405 410 415	1247
AGT GAC AAG AAG TTT CAG CGG CCT CAA GAT CAG TAC CCA CCT TTC CGC Ser Asp Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro Phe Arg	1295

	420	425	430	
TTC GGC ACG GTG CCC AAC GGC AGC ACG GAG CGG AAC ATC CGC AGT AAC Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Ser Asn	435	440	445	1343
TAC CGT GAC ATG CAC ACC CAC ATG GTC AAG TTC AAC CAG CGC TCG GTG Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg Ser Val	450	455	460	1391
GAG GAC GCG CTC ACC AGC CTC AAG ATG GGC AAG GAC GAG GGC TGC AAG Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp Glu Gly Cys Lys	465	470	475	1439
CTG GTC ACC ATT GGG TCT GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly	480	485	490	1487
ATC GCC ATG CAG AAG GAC TCC CAC TGG AAG CGG GCC ATA GAC CTG GCG Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala	500	505	510	1535
CTC TTG CAG TTC CTG GGG GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val	515	520	525	1583
TGG CTC TCA GGG ATC TGC CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser	530	535	540	1631
AAG CTG GAC ATC GAC AAC ATG GGA GGC GTC TTC TAC ATG CTG CTG GTG Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val	545	550	555	1679
GCC ATG GGG CTG GCC CTG CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr	560	565	570	1727
TGG AAG CTG CGC CAC TCG GTG CCC AAC TCA TCC CAG CTG GAC TTC CTG Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu	580	585	590	1775
CTG GCT TTC AGC AGG GGC ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser	595	600	605	1823
CTC GCC AGC CCA CCG CGG CAG GCC AGC CCG GAC CTC ACG GCC AGC TCG Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser	610	615	620	1871
GCC CAG GCC AGC GTG CTC AAG ATT CTG CAG GCA GCC CGC GAC ATG GTG Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val	625	630	635	1919
ACC ACG GCG GGC GTA AGC AAC TCC CTG GAC CGC GCC ACT CGC ACC ATC Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile	640	645	650	1967
GAG AAT TGG GGT GGC GGC CGC CGT GCG CCC CCA CCG TCC CCC TGC CCG Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro	660	665	670	2015
ACC CCG CGG TCT GGC CCC AGC CCA TGC CTG CCC ACC CCC GAC CCG CCC Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro	675	680	685	2063
CCA GAG CCG AGC CCC ACG GGC TGG GGA CCG CCA GAC GGG GGT CGC GCG				2111

Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala		
690	695	700
GCG CTT GTG CGC AGG GCT CCG CAG CCC CCG GGC CGC CCC CCG ACG CCG		2159
Ala Leu Val Arg Arg Ala Pro Gln Pro Gly Arg Pro Pro Thr Pro		
705	710	715
GGG CCG CCC CTG TCC GAC GTC TCC CGA GTG TCG CGC CGC CCA GCC TGG		2207
Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp		
720	725	730
735		
GAG GCG CGG TGG CCG GTG CGG ACC GGG CAC TGC GGG AGG CAC CTC TCG		2255
Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser		
740	745	750
GCC TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT CAC TAC AGC TCC TTT		2303
Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe		
755	760	765
CCT CGA GCC GAC CGA TCC GGC CG		2326
Pro Arg Ala Asp Arg Ser Gly		
770		

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 774 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly His Val Trp Leu Val Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala		
1	5	10
15		
Pro Pro Ala Thr Phe Pro Val Gly Leu Ile Ser Val Val Thr Glu Ser		
20	25	30
30		
Trp Arg Leu Ser Leu Arg Gln Lys Val Arg Asp Gly Val Ala Ile Leu		
35	40	45
45		
Ala Leu Gly Ala His Ser Tyr Trp Arg Gln His Gly Thr Leu Pro Ala		
50	55	60
60		
Pro Ala Gly Asp Cys Arg Val His Pro Gly Pro Val Ser Pro Ala Arg		
65	70	75
75		
80		
Glu Ala Phe Tyr Arg His Leu Leu Asn Val Thr Trp Glu Gly Arg Asp		
85	90	95
95		
Phe Ser Phe Ser Pro Gly Gly Tyr Leu Val Gln Pro Thr Met Val Val		
100	105	110
110		
Ile Ala Leu Asn Arg His Arg Leu Trp Glu Met Val Gly Arg Trp Glu		
115	120	125
125		
His Gly Val Leu Tyr Met Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala		
130	135	140
140		
Ser Leu Gln Pro Val Val Asp Ser Arg His Leu Thr Val Ala Thr Leu		
145	150	155
155		
160		
Glu Glu Arg Pro Phe Val Ile Val Glu Ser Pro Asp Pro Gly Thr Gly		
165	170	175
175		

Gly Cys Val Pro Asn Thr Val Pro Cys Arg Arg Gln Ser Asn His Thr  
180 185 190

Phe Ser Ser Gly Asp Val Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly  
195 200 205

Phe Cys Ile Asp Ile Leu Lys Lys Leu Ala Arg Val Val Lys Phe Ser  
210 215 220

Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys Arg Val Arg  
225 230 235 240

Gly Val Trp Asn Gly Met Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp  
245 250 255

Met Ala Ile Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser Glu Ile Val  
260 265 270

Asp Phe Ser Val Pro Phe Val Glu Thr Gly Ile Ser Val Met Val Ala  
275 280 285

Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser  
290 295 300

Pro Ala Val Trp Val Met Met Phe Val Met Cys Leu Thr Val Val Ala  
305 310 315 320

Ile Thr Val Phe Met Phe Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln  
325 330 335

Asn Leu Thr Arg Gly Lys Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly  
340 345 350

Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn Ser Val Pro  
355 360 365

Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val Leu Val Trp  
370 375 380

Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala  
385 390 395 400

Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser  
405 410 415

Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe  
420 425 430

Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr  
435 440 445

Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg Ser Val Glu  
450 455 460

Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp Glu Gly Cys Lys Leu  
465 470 475 480

Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile  
485 490 495

Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu  
500 505 510

Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp  
515 520 525

Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys  
530 535 540

Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val Ala  
545 550 555 560

Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp  
565 570 575

Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu  
580 585 590

Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu  
595 600 605

Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala  
610 615 620

Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr  
625 630 635 640

Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu  
645 650 655

Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr  
660 665 670

Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro  
675 680 685

Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala  
690 695 700

Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly  
705 710 715 720

Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu  
725 730 735

Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala  
740 745 750

Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro  
755 760 765

Arg Ala Asp Arg Ser Gly  
770

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3698 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 3...3698

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

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TG GAG ATC CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC Glu Ile Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser 1 5 10 15	47
AGC CTC CTC ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC Ser Leu Leu Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His 20 25 30	95
GGC ATT GTC TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC Gly Ile Val Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile 35 40 45	143
CTT GAC TTC ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC Leu Asp Phe Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser 50 55 60	191
GGA GGC TCT GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC Gly Gly Ser Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe 65 70 75	239
CTG CAG CTG GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG Leu Gln Leu Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys 80 85 90 95	287
GTG CTG GAA GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG Val Leu Glu Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu 100 105 110	335
CAC CCG GGC CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC His Pro Gly His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp 115 120 125	383
GCC AGC CAC GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG Ala Ser His Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu 130 135 140	431
GAC CCG GGA GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC Asp Pro Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu 145 150 155	479
GAC GCG CCC GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG Asp Ala Pro Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val 160 165 170 175	527
CTC TTC GCC GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG Leu Phe Ala Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val 180 185 190	575
TGG CTG GTG CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC Trp Leu Val Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala 195 200 205	623
ACC TTC CCC GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC Thr Phe Pro Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu 210 215 220	671
AGC CTG CGC CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC Ser Leu Arg Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly 225 230 235	719
GCC CAC AGC TAC TGG CGC CAG CAT GGA ACC CAG AAG GGG GTG TGC CAG Ala His Ser Tyr Trp Arg Gln His Gly Thr Gln Lys Gly Val Cys Gln 240 245 250 255	767
CCC CGG CCG GGG ACT GCC GTG TTC ACC CTG GGC CCG TCA GCC CTG CCC Pro Arg Pro Gly Thr Ala Val Phe Thr Leu Gly Pro Ser Ala Leu Pro 260 265 270	815

GGG AGG CCT TCT ACA GGC ACC TAC TGA ATG TCA CCT GGG AGG GCC GAG Gly Arg Pro Ser Thr Gly Thr Tyr * Met Ser Pro Gly Arg Ala Glu 275 280 285	863
ACT TCT CCT TCA GCC CTG GTG GGT ACC TGG TCC AGC CCA CCA TGG TGG Thr Ser Pro Ser Ala Leu Val Gly Thr Trp Ser Ser Pro Pro Trp Trp 290 295 300	911
TGA TCG CCC TCA ACC GGC ACC GCC TCT GGG AGA TGG TGG GGC GCT GGG * Ser Pro Ser Thr Gly Thr Ala Ser Gly Arg Trp Trp Gly Ala Gly 305 310 315	959
AGC ATG GCG TCC TAT ACA TGA AGT ACC CCG TGT GGC CTC GCT ACA GTG Ser Met Ala Ser Tyr Thr * Ser Thr Pro Cys Gly Leu Ala Thr Val 320 325 330 335	1007
CCT CTC TGC AGC CTG TGG TGG ACA GTC GGC ACC TGA CGG TGG CCA CGC Pro Leu Cys Ser Leu Trp Trp Thr Val Gly Thr * Arg Trp Pro Arg 340 345 350	1055
TGG AAG AGC GGC CCT TTG TCA TCG TGG AGA GCC CTG ACC CTG GCA CAG Trp Lys Ser Gly Pro Leu Ser Ser Trp Arg Ala Leu Thr Leu Ala Gln 355 360 365	1103
GAG GCT GTG TCC CCA ACA CCG TGC CCT GCC GCA GGC AGA GCA ACC ACA Glu Ala Val Ser Pro Thr Pro Cys Pro Ala Ala Gly Arg Ala Thr Thr 370 375 380	1151
CCT TCA GCA GCG GGG ACG TGG CCC CCT ACA CCA AGC TCT GCT GTA AGG Pro Ser Ala Ala Gly Thr Trp Pro Pro Thr Pro Ser Ser Ala Val Arg 385 390 395	1199
GAT TCT GCA TCG ACA TCC TCA AGA AGC TGG CCA GAG TGG TCA AAT TCT Asp Ser Ala Ser Thr Ser Arg Ser Trp Pro Glu Trp Ser Asn Ser 400 405 410 415	1247
CCT ACG ACC TGT ACC TGG TGA CCA ACG GCA AGC ATG GCA AGC GGG TGC Pro Thr Thr Cys Thr Trp * Pro Thr Ala Ser Met Ala Ser Gly Cys 420 425 430	1295
GCG GCG TAT GGA ACG GCA TGA TTG GGG AGG TGT ACT ACA AGC GGG CAG Ala Ala Tyr Gly Thr Ala * Leu Gly Arg Cys Thr Thr Ser Gly Gln 435 440 445	1343
ACA TGG CCA TCG GCT CCC TCA CCA TCA ATG AGG AAC GCT CCG AGA TCG Thr Trp Pro Ser Ala Pro Ser Pro Ser Met Arg Asn Ala Pro Arg Ser 450 455 460	1391
TAG ACT TCT CTG TAC CCT TTG TGG AGA CGG GCA TCA GTG TGA TGG TGG * Thr Ser Leu Tyr Pro Leu Trp Arg Arg Ala Ser Val * Trp Trp 465 470 475	1439
CTC GCA GCA ATG GCA CCG TCT CCC CCT CGG CCT TCT TGG AGC CAT ATA Leu Ala Ala Met Ala Pro Ser Pro Pro Arg Pro Ser Trp Ser His Ile 480 485 490 495	1487
GCC CTG CAG TGT GGG TGA TGA TGT TTG TCA TGT GCC TCA CTG TGG TGG Ala Leu Gln Cys Gly * * Cys Leu Ser Cys Ala Ser Leu Trp Trp 500 505 510	1535
CCA TCA CCG TCT TCA TGT TCG AGT ACT TCA GCC CTG TCA GCT ACA ACC Pro Ser Pro Ser Ser Cys Ser Ser Thr Ser Ala Leu Ser Ala Thr Thr 515 520 525	1583
AGA ACC TCA CCA GAG GCA AGA CTT TCA CTA TCG GCA AGT CCG TGT GGC Arg Thr Ser Pro Glu Ala Arg Leu Ser Leu Ser Ala Ser Pro Cys Gly 530 535 540	1631

TGC	TGT	GGG	CGC	TGG	TCT	TCA	ACA	ACT	CAG	TGC	CCA	TCG	AGA	ACC	CGC	1679
Cys	Cys	Gly	Arg	Trp	Ser	Ser	Thr	Thr	Gln	Cys	Pro	Ser	Arg	Thr	Arg	
545					550					555						
GGG	GCA	CCA	CCA	GCA	AGA	TCA	TGG	TTC	TGG	TCT	GGG	CCT	TCT	TTG	CTG	1727
Gly	Ala	Pro	Pro	Ala	Arg	Ser	Trp	Phe	Trp	Ser	Gly	Pro	Ser	Leu	Leu	
560					565				570					575		
TCA	TCT	TCC	TCG	CCA	GAT	ACA	CGG	CCA	ACC	TGG	CCG	CCT	TCA	TGA	TCC	1775
Ser	Ser	Ser	Pro	Asp	Thr	Arg	Pro	Thr	Trp	Pro	Pro	Ser	*	Ser		
					580			585					590			
AAG	AGC	AAT	ACA	TCG	ACA	CTG	TGT	CGG	GCC	TCA	GTG	ACA	AGA	AGT	TTC	1823
Lys	Ser	Asn	Thr	Ser	Thr	Leu	Cys	Arg	Ala	Ser	Val	Thr	Arg	Ser	Phe	
					595			600					605			
AGC	GCG	CTC	AAG	ATC	AGT	ACC	CAC	CTT	TCC	GCT	TCG	GCA	CGG	TGC	CCA	1871
Ser	Gly	Leu	Lys	Ile	Ser	Thr	His	Leu	Ser	Ala	Ser	Ala	Arg	Cys	Pro	
					610			615					620			
ACG	GCA	GCA	CGG	AGC	GGA	ACA	TCC	GCA	GTA	ACT	ACC	GTG	ACA	TGC	ACA	1919
Thr	Ala	Ala	Arg	Ser	Gly	Thr	Ser	Ala	Val	Thr	Thr	Val	Thr	Cys	Thr	
					625			630					635			
CCC	ACA	TGG	TCA	AGT	TCA	ACC	AGC	GCT	CGG	TGG	AGG	ACG	CGC	TCA	CCA	1967
Pro	Thr	Trp	Ser	Ser	Ser	Thr	Ser	Ala	Arg	Trp	Arg	Thr	Arg	Ser	Pro	
					640			645					650		655	
GCC	TCA	AGA	TGG	GGA	AGC	TGG	ATG	CCT	TCA	TCT	ATG	ATG	CTG	CTG	TCC	2015
Ala	Ser	Arg	Trp	Gly	Ser	Trp	Met	Pro	Ser	Ser	Met	Met	Leu	Leu	Ser	
					660			665					670			
TCA	ACT	ACA	TGG	CAG	GCA	AGG	ACG	AGG	GCT	GCA	AGC	TGG	TCA	CCA	TTG	2063
Ser	Thr	Thr	Trp	Gln	Ala	Arg	Thr	Arg	Ala	Ala	Ser	Trp	Ser	Pro	Leu	
					675			680					685			
GGT	CTG	GCA	AGG	TCT	TTG	CTA	CCA	CTG	GCT	ACG	GCA	TCG	CCA	TGC	AGA	2111
Gly	Leu	Ala	Arg	Ser	Leu	Leu	Pro	Leu	Ala	Thr	Ala	Ser	Pro	Cys	Arg	
					690			695					700			
AGG	ACT	CCC	ACT	GGA	AGC	GGG	CCA	TAG	ACC	TGG	CGC	TCT	TGC	AGT	TCC	2159
Arg	Thr	Pro	Thr	Gly	Ser	Gly	Pro	*	Thr	Trp	Arg	Ser	Cys	Ser	Ser	
					705			710					715			
TGG	GGG	ACG	GAG	AGA	CAC	AGA	AAC	TGG	AGA	CAG	TGT	GGC	TCT	CAG	GGA	2207
Trp	Gly	Thr	Glu	Arg	His	Arg	Asn	Trp	Arg	Gln	Cys	Gly	Ser	Gln	Gly	
					720			725					730		735	
TCT	GCC	AGA	ATG	AGA	AGA	ACG	AGG	TGA	TGA	GCA	GCA	AGC	TGG	ACA	TCG	2255
Ser	Ala	Arg	Met	Arg	Arg	Thr	Arg	*	*	Ala	Ala	Ser	Trp	Thr	Ser	
					740			745					750			
ACA	ACA	TGG	GAG	GCG	TCT	TCT	ACA	TGC	TGC	TGG	TGG	CCA	TGG	GGC	TGG	2303
Thr	Thr	Trp	Glu	Ala	Ser	Ser	Thr	Cys	Cys	Trp	Trp	Pro	Trp	Gly	Trp	
					755			760					765			
CCC	TGC	TGG	TCT	TCG	CCT	GGG	AGC	ACC	TGG	TCT	ACT	GGA	AGC	TGC	GCC	2351
Pro	Cys	Trp	Ser	Ser	Pro	Gly	Ser	Thr	Trp	Ser	Thr	Gly	Ser	Cys	Ala	
					770			775					780			
ACT	CGG	TGC	CCA	ACT	CAT	CCC	AGC	TGG	ACT	TCC	TGC	TGG	CTT	TCA	GCA	2399
Thr	Arg	Cys	Pro	Thr	His	Pro	Ser	Trp	Thr	Ser	Cys	Trp	Leu	Ser	Ala	
					785			790					795			
GGG	GCA	TCT	ACA	GCT	GCT	TCA	GCG	GGG	TGC	AGA	GCC	TCG	CCA	GCC	CAC	2447
Gly	Ala	Ser	Thr	Ala	Ala	Ser	Ala	Gly	Cys	Arg	Ala	Ser	Pro	Ala	His	
					800			805					810		815	

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CGC GGC AGG CCA GCC CGG ACC TCA CGG CCA GCT CGG CCC AGG CCA GCG	2495
Arg Gly Arg Pro Ala Arg Thr Ser Arg Pro Ala Arg Pro Arg Pro Ala	
820 825 830	
TGC TCA AGA TTC TGC AGG CAG CCC GCG ACA TGG TGA CCA CGG CGG GCG	2543
Cys Ser Arg Phe Cys Arg Gln Pro Ala Thr Trp * Pro Arg Arg Ala	
835 840 845	
TAA GCA ACT CCC TGG ACC GCG CCA CTC GCA CCA TCG AGA ATT GGG GTG	2591
* Ala Thr Pro Trp Thr Ala Pro Leu Ala Pro Ser Arg Ile Gly Val	
850 855 860	
GCG GCC GCC GTG CGC CCC CAC CGT CCC CCT GCC CGA CCC CGC GGT CTG	2639
Ala Ala Ala Val Arg Pro His Arg Pro Pro Ala Arg Pro Arg Gly Leu	
865 870 875	
GCC CCA GCC CAT GCC TGC CCA CCC CCG ACC CGC CCC CAG AGC CGA GCC	2687
Ala Pro Ala His Ala Cys Pro Pro Pro Thr Arg Pro Gln Ser Arg Ala	
880 885 890 895	
CCA CGG GCT GGG GAC CGC CAG ACG GGG GTC GCG CGG CGC TTG TGC GCA	2735
Pro Arg Ala Gly Asp Arg Gln Thr Gly Val Ala Arg Arg Leu Cys Ala	
900 905 910	
GGG CTC CGC AGC CCC CGG GCC GCC CCC CGA CGC CGG GGC CGC CCC TGT	2783
Gly Leu Arg Ser Pro Arg Ala Ala Pro Arg Arg Arg Gly Arg Pro Cys	
915 920 925	
CCG ACG TCT CCC GAG TGT CGC GCC GCC CAG CCT GGG AGG CGC GGT GGC	2831
Pro Thr Ser Pro Glu Cys Arg Ala Ala Gln Pro Gly Arg Arg Gly Gly	
930 935 940	
CGG TGC GGA CCG GGC ACT GCG GGA GGC ACC TCT CGG CCT CCG AGC GGC	2879
Arg Cys Gly Pro Gly Thr Ala Gly Gly Thr Ser Arg Pro Pro Ser Gly	
945 950 955	
CCC TGT CGC CCG CGC GCT GTC ACT ACA GCT CCT TTC CTC GAG CCG ACC	2927
Pro Cys Arg Pro Arg Ala Val Thr Thr Ala Pro Phe Leu Glu Pro Thr	
960 965 970 975	
GAT CCG GCC GCC CCT TCC TCC CGC TCT TCC CGG AGC CCC CGG AGC TGG	2975
Asp Pro Ala Ala Pro Ser Ser Arg Ser Ser Arg Ser Pro Arg Ser Trp	
980 985 990	
AGG ACC TGC CGC TGC TCG GTC CGG AGC AGC TGG CCC GGC GGG AGG CCC	3023
Arg Thr Cys Arg Cys Ser Val Arg Ser Ser Trp Pro Gly Gly Arg Pro	
995 1000 1005	
TGC TGA ACG CGG CCT GGG CCC GGG GCT CGC GCC CGA GTC ACG CTT CCC	3071
Cys * Thr Arg Pro Gly Pro Gly Ala Arg Ala Arg Val Thr Leu Pro	
1010 1015 1020	
TGC CCA GCT CCG TGG CCG AGG CCT TCG CTC GGC CCA GCT CGC TGC CCG	3119
Cys Pro Ala Pro Trp Pro Arg Pro Ser Leu Gly Pro Ala Arg Cys Pro	
1025 1030 1035	
CTG GGT GCA CCG GCC CCG CCT GCG CCC GCC CCG ACG GCC ACT CGG CCT	3167
Leu Gly Ala Pro Ala Pro Pro Ala Pro Ala Pro Thr Ala Thr Arg Pro	
1040 1045 1050 1055	
GCA GGC GCT TGG CGC AGG CGC AGT CGA TGT GCT TGC CGA TCT ACC GGG	3215
Ala Gly Ala Trp Arg Arg Ser Arg Cys Ala Cys Arg Ser Thr Gly	
1060 1065 1070 1075	
AGG CCT GCC AGG AGG GCG AGC AGG CAG GGG CCC CCG CCT GGC AGC ACA	3263
Arg Pro Ala Arg Arg Ala Ser Arg Gln Gly Pro Pro Gly Ser Thr	
1075 1080 1085	

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GAC AGC ACG TCT GCC TGC ACG CCC ACG CCC ACC TGC CAT TGT GCT GGG	3311
Asp Ser Thr Ser Ala Cys Thr Pro Thr Pro Thr Cys His Cys Ala Gly	
1090 1095 1100	
GGG CTG TCT GTC CTC ACC TTC CAC CCT GTG ACA GCC ACG GCT CCT GGC	3359
Gly Leu Ser Val Leu Thr Phe His Pro Val Thr Ala Thr Ala Pro Gly	
1105 1110 1115	
TCT CCG GCG CCT GGG GGC CTC TGG GGC ACA GCG GCA GGA CTC TGG GGC	3407
Ser Pro Ala Pro Gly Gly Leu Trp Gly Thr Ala Ala Gly Leu Trp Gly	
1120 1125 1130 1135	
TGG GCA CAG GCT ACA GAG ACA GTG GGG GAC TGG ACG AGA TCA GCA GTG	3455
Trp Ala Gln Ala Thr Glu Thr Val Gly Asp Trp Thr Arg Ser Ala Val	
1140 1145 1150	
TAG CCC GTG GGA CGC AAG GCT TCC CGG GAC CCT GCA CCT GGA GAC GGA	3503
* Pro Val Gly Arg Lys Ala Ser Arg Asp Pro Ala Pro Gly Asp Gly	
1155 1160 1165	
TCT CCA GTC TGG AGT CAG AAG TGT GAG TTA TCA GCC ACT CAG GCT CCG	3551
Ser Pro Val Trp Ser Gln Lys Cys Glu Leu Ser Ala Thr Gln Ala Pro	
1170 1175 1180	
AGC CAG CTG GAT TCT CTG CCT GCC ACT GTC AGG GTT AAG CGG CAG GCA	3599
Ser Gln Leu Asp Ser Leu Pro Ala Thr Val Arg Val Lys Arg Gln Ala	
1185 1190 1195	
GGA TTG GCC CTT CTC TGG CTT CTA CCA TGA AAT CCT GGC CAT GGC ACC	3647
Gly Leu Ala Leu Leu Trp Leu Leu Pro * Asn Pro Gly His Gly Thr	
1200 1205 1210 1215	
CCA GTG ACA GAT GAT GTC TTC CAT GGT CAT CAG TGA CCT CAG CTA GCC	3695
Pro Val Thr Asp Asp Val Phe His Gly His Gln * Pro Gln Leu Ala	
1220 1225 1230	
TCA	3698
Ser	

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: unknown  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
(A) NAME/KEY: Coding Sequence  
(B) LOCATION: 1...3243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTC GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC GAG GCG	48
Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala	
1 5 10 15	
GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG CCC AAC	96
Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn	
20 25 30	
CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC GTG GGC	144

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Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly		
35	40	45
CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC CAG AAG		192
Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys		
50	55	60
GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC TAC TGG		240
Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp		
65	70	75
CGC CAG CAT GGA ACC CAG AAG GGG GTG TGC CAG CCC CGG CCG GGG ACT		288
Arg Gln His Gly Thr Gln Lys Gly Val Cys Gln Pro Arg Pro Gly Thr		
85	90	95
GCC GTG TTC ACC CTG GGC CCG TCA GCC CTG CCC GGG AGG CCT TCT ACA		336
Ala Val Phe Thr Leu Gly Pro Ser Ala Leu Pro Gly Arg Pro Ser Thr		
100	105	110
GGC ACC TAC TGA ATG TCA CCT GGG AGG GCC GAG ACT TCT CCT TCA GCC		384
Gly Thr Tyr * Met Ser Pro Gly Arg Ala Glu Thr Ser Pro Ser Ala		
115	120	125
CTG GTG GGT ACC TGG TCC AGC CCA CCA TGG TGG TGA TCG CCC TCA ACC		432
Leu Val Gly Thr Trp Ser Ser Pro Pro Trp Trp * Ser Pro Ser Thr		
130	135	140
GGC ACC GCC TCT GGG AGA TGG TGG GGC GCT GGG AGC ATG GCG TCC TAT		480
Gly Thr Ala Ser Gly Arg Trp Trp Gly Ala Gly Ser Met Ala Ser Tyr		
145	150	155
ACA TGA AGT ACC CCG TGT GGC CTC GCT ACA GTG CCT CTC TGC AGC CTG		528
Thr * Ser Thr Pro Cys Gly Leu Ala Thr Val Pro Leu Cys Ser Leu		
165	170	175
TGG TGG ACA GTC GGC ACC TGA CGG TGG CCA CGC TGG AAG AGC GGC CCT		576
Trp Trp Thr Val Gly Thr * Arg Trp Pro Arg Trp Lys Ser Gly Pro		
180	185	190
TTG TCA TCG TGG AGA GCC CTG ACC CTG GCA CAG GAG GCT GTG TCC CCA		624
Leu Ser Ser Trp Arg Ala Leu Thr Leu Ala Gln Glu Ala Val Ser Pro		
195	200	205
ACA CCG TGC CCT GCC GCA GGC AGA GCA ACC ACA CCT TCA GCA GCG GGG		672
Thr Pro Cys Pro Ala Ala Gly Arg Ala Thr Thr Pro Ser Ala Ala Gly		
210	215	220
ACG TGG CCC CCT ACA CCA AGC TCT GCT GTA AGG GAT TCT GCA TCG ACA		720
Thr Trp Pro Pro Thr Pro Ser Ser Ala Val Arg Asp Ser Ala Ser Thr		
225	230	235
240		
TCC TCA AGA AGC TGG CCA GAG TGG TCA AAT TCT CCT ACG ACC TGT ACC		768
Ser Ser Arg Ser Trp Pro Glu Trp Ser Asn Ser Pro Thr Thr Cys Thr		
245	250	255
TGG TGA CCA ACG GCA AGC ATG GCA AGC GGG TGC GCG GCG TAT GGA ACG		816
Trp * Pro Thr Ala Ser Met Ala Ser Gly Cys Ala Ala Tyr Gly Thr		
260	265	270
GCA TGA TTG GGG AGG TGT ACT ACA AGC GGG CAG ACA TGG CCA TCG GCT		864
Ala * Leu Gly Arg Cys Thr Thr Ser Gly Gln Thr Trp Pro Ser Ala		
275	280	285
CCC TCA CCA TCA ATG AGG AAC GCT CCG AGA TCG TAG ACT TCT CTG TAC		912
Pro Ser Pro Ser Met Arg Asn Ala Pro Arg Ser * Thr Ser Leu Tyr		
290	295	300

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CCT TTG TGG AGA CGG GCA TCA GTG TGA TGG TGG CTC GCA GCA ATG GCA Pro Leu Trp Arg Arg Ala Ser Val * Trp Trp Leu Ala Ala Met Ala 305 310 315 320	960
CCG TCT CCC CCT CGG CCT TCT TGG AGC CAT ATA GCC CTG CAG TGT GGG Pro Ser Pro Pro Arg Pro Ser Trp Ser His Ile Ala Leu Gln Cys Gly 325 330 335	1008
TGA TGA TGT TTG TCA TGT GCC TCA CTG TGG TGG CCA TCA CCG TCT TCA * * Cys Leu Ser Cys Ala Ser Leu Trp Trp Pro Ser Pro Ser Ser 340 345 350	1056
TGT TCG AGT ACT TCA GCC CTG TCA GCT ACA ACC AGA ACC TCA CCA GAG Cys Ser Ser Thr Ser Ala Leu Ser Ala Thr Thr Arg Thr Ser Pro Glu 355 360 365	1104
GCA AGA AGT CCG GGG GCC CAG CTT TCA CTA TCG GCA AGT CCG TGT GGC Ala Arg Ser Pro Gly Ala Gln Leu Ser Leu Ser Ala Ser Pro Cys Gly 370 375 380	1152
TGC TGT GGG CGC TGG TCT TCA ACA ACT CAG TGC CCA TCG AGA ACC CGC Cys Cys Gly Arg Trp Ser Ser Thr Thr Gln Cys Pro Ser Arg Thr Arg 385 390 395 400	1200
GGG GCA CCA CCA GCA AGA TCA TGG TTC TGG TCT GGG CCT TCT TTG CTG Gly Ala Pro Pro Ala Arg Ser Trp Phe Trp Ser Gly Pro Ser Leu Leu 405 410 415	1248
TCA TCT TCC TCG CCA GAT ACA CGG CCA ACC TGG CCG CCT TCA TGA TCC Ser Ser Ser Pro Asp Thr Arg Pro Thr Trp Pro Pro Ser * Ser 420 425 430	1296
AAG AGC AAT ACA TCG ACA CTG TGT CGG GCC TCA GTG ACA AGA AGT TTC Lys Ser Asn Thr Ser Thr Leu Cys Arg Ala Ser Val Thr Arg Ser Phe 435 440 445	1344
AGC GGC CTC AAG ATC AGT ACC CAC CTT TCC GCT TCG GCA CGG TGC CCA Ser Gly Leu Lys Ile Ser Thr His Leu Ser Ala Ser Ala Arg Cys Pro 450 455 460	1392
ACG GCA GCA CGG AGC GGA ACA TCC GCA GTA ACT ACC GTG ACA TGC ACA Thr Ala Ala Arg Ser Gly Thr Ser Ala Val Thr Thr Val Thr Cys Thr 465 470 475 480	1440
CCC ACA TGG TCA AGT TCA ACC AGC GCT CGG TGG AGG ACG CGC TCA CCA Pro Thr Trp Ser Ser Thr Ser Ala Arg Trp Arg Thr Arg Ser Pro 485 490 495	1488
GCC TCA AGA TGG GCT CTG AGG CTC AGC CTG TCC CCA GGA AGC TGG ATG Ala Ser Arg Trp Ala Leu Arg Leu Ser Leu Ser Pro Gly Ser Trp Met 500 505 510	1536
CCT TCA TCT ATG ATG CTG CTG TCC TCA ACT ACA TGG CAG GCA AGG ACG Pro Ser Ser Met Met Leu Leu Ser Ser Thr Thr Trp Gln Ala Arg Thr 515 520 525	1584
AGG GCT GCA AGC TGG TCA CCA TTG GGT CTG GCA AGG TCT TTG CTA CCA Arg Ala Ala Ser Trp Ser Pro Leu Gly Leu Ala Arg Ser Leu Leu Pro 530 535 540	1632
CTG GCT ACG GCA TCG CCA TGC AGA AGG ACT CCC ACT GGA AGC GGG CCA Leu Ala Thr Ala Ser Pro Cys Arg Arg Thr Pro Thr Gly Ser Gly Pro 545 550 555 560	1680
TAG ACC TGG CGC TCT TGC AGT TCC TGG GGG ACG GAG AGA CAC AGA AAC * Thr Trp Arg Ser Cys Ser Ser Trp Gly Thr Glu Arg His Arg Asn 565 570 575	1728

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TGG AGA CAG TGT GGC TCT CAG GGA TCT GCC AGA ATG AGA AGA ACG AGG Trp Arg Gln Cys Gly Ser Gln Gly Ser Ala Arg Met Arg Arg Thr Arg 580 585 590	1776
TGA TGA GCA GCA AGC TGG ACA TCG ACA ACA TGG GAG GCG TCT TCT ACA * * Ala Ala Ser Trp Thr Ser Thr Trp Glu Ala Ser Ser Thr 595 600 605	1824
TGC TGC TGG TGG CCA TGG GGC TGG CCC TGC TGG TCT TCG CCT GGG AGC Cys Cys Trp Trp Pro Trp Gly Trp Pro Cys Trp Ser Ser Pro Gly Ser 610 615 620	1872
ACC TGG TCT ACT GGA AGC TGC GCC ACT CGG TGC CCA ACT CAT CCC AGC Thr Trp Ser Thr Gly Ser Cys Ala Thr Arg Cys Pro Thr His Pro Ser 625 630 635 640	1920
TGG ACT TCC TGC TGG CTT TCA GCA GGG GCA TCT ACA GCT GCT TCA GCG Trp Thr Ser Cys Trp Leu Ser Ala Gly Ala Ser Thr Ala Ala Ser Ala 645 650 655	1968
GGG TGC AGA GCC TCG CCA GCC CAC CGC GGC AGG CCA GCC CGG ACC TCA Gly Cys Arg Ala Ser Pro Ala His Arg Gly Arg Pro Ala Arg Thr Ser 660 665 670	2016
CGG CCA GCT CGG CCC AGG CCA GCG TGC TCA AGA TTC TGC AGG CAG CCC Arg Pro Ala Arg Pro Arg Pro Ala Cys Ser Arg Phe Cys Arg Gln Pro 675 680 685	2064
GCG ACA TGG TGA CCA CGG CGG GCG TAA GCA ACT CCC TGG ACC GCG CCA Ala Thr Trp * Pro Arg Arg Ala * Ala Thr Pro Trp Thr Ala Pro 690 695 700	2112
CTC GCA CCA TCG AGA ATT GGG GTG GCG GCC GCC GTG CGC CCC CAC CGT Leu Ala Pro Ser Arg Ile Gly Val Ala Ala Val Arg Pro His Arg 705 710 715 720	2160
CCC CCT GCC CGA CCC CGC GGT CTG GCC CCA GCC CAT GCC TGC CCA CCC Pro Pro Ala Arg Pro Arg Gly Leu Ala Pro Ala His Ala Cys Pro Pro 725 730 735	2208
CCG ACC CGC CCC CAG AGC CGA GCC CCA CGG GCT GGG GAC CGC CAG ACG Pro Thr Arg Pro Gln Ser Arg Ala Pro Arg Ala Gly Asp Arg Gln Thr 740 745 750	2256
GGG GTC GCG CGG CGC TTG TGC GCA GGG CTC CGC AGC CCC CGG GCC GCC Gly Val Ala Arg Arg Leu Cys Ala Gly Leu Arg Ser Pro Arg Ala Ala 755 760 765	2304
CCC CGA CGC CGG GGC CGC CCC TGT CCG ACG TCT CCC GAG TGT CGC GCC Pro Arg Arg Arg Gly Arg Pro Cys Pro Thr Ser Pro Glu Cys Arg Ala 770 775 780	2352
GCC CAG CCT GGG AGG CGC GGT GGC CGG TGC GGA CCG GGC ACT GCG GGA Ala Gln Pro Gly Arg Arg Gly Arg Cys Gly Pro Gly Thr Ala Gly 785 790 795 800	2400
GGC ACC TCT CGG CCT CCG AGC GGC CCC TGT CGC CCG CGC GCT GTC ACT Gly Thr Ser Arg Pro Pro Ser Gly Pro Cys Arg Pro Arg Ala Val Thr 805 810 815	2448
ACA GCT CCT TTC CTC GAG CCG ACC GAT CCG GCC GCC CCT TCC TCC CGC Thr Ala Pro Phe Leu Glu Pro Thr Asp Pro Ala Ala Pro Ser Ser Arg 820 825 830	2496
TCT TCC CGG AGC CCC CGG AGC TGG AGG ACC TGC CGC TGC TCG GTC CGG Ser Ser Arg Ser Pro Arg Ser Trp Arg Thr Cys Arg Cys Ser Val Arg 835 840 845	2544

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AGC AGC TGG CCC GGC GGG AGG CCC TGC TGA ACG CGG CCT GGG CCC GGG Ser Ser Trp Pro Gly Gly Arg Pro Cys * Thr Arg Pro Gly Pro Gly	850	855	860	2592
GCT CGC GCC CGA GTC ACG CTT CCC TGC CCA GCT CCG TGG CCG AGG CCT Ala Arg Ala Arg Val Thr Leu Pro Cys Pro Ala Pro Trp Pro Arg Pro	865	870	875	880
TCG CTC GGC CCA GCT CGC TGC CCG CTG GGT GCA CCG GCC CCG CCT GCG Ser Leu Gly Pro Ala Arg Cys Pro Leu Gly Ala Pro Ala Pro Pro Ala	885	890	895	2688
CCC GCC CCG ACG GCC ACT CGG CCT GCA GGC GCT TGG CGC AGG CGC AGT Pro Ala Pro Thr Ala Thr Arg Pro Ala Gly Ala Trp Arg Arg Arg Ser	900	905	910	2736
CGA TGT GCT TGC CGA TCT ACC GGG AGG CCT GCC AGG AGG GCG AGC AGG Arg Cys Ala Cys Arg Ser Thr Gly Arg Pro Ala Arg Arg Ala Ser Arg	915	920	925	2784
CAG GGG CCC CCG CCT GGC AGC ACA GAC AGC ACG TCT GCC TGC ACG CCC Gln Gly Pro Pro Pro Gly Ser Thr Asp Ser Thr Ser Ala Cys Thr Pro	930	935	940	2832
ACG CCC ACC TGC CAT TGT GCT GGG GGG CTG TCT GTC CTC ACC TTC CAC Thr Pro Thr Cys His Cys Ala Gly Gly Leu Ser Val Leu Thr Phe His	945	950	955	2880
CCT GTG ACA GCC ACG GCT CCT GGC TCT CCG GCG CCT GGG GGC CTC TGG Pro Val Thr Ala Thr Ala Pro Gly Ser Pro Ala Pro Gly Gly Leu Trp	965	970	975	2928
GGC ACA GCG GCA GGA CTC TGG GGC TGG GCA CAG GCT ACA GAG ACA GTG Gly Thr Ala Ala Gly Leu Trp Gly Trp Ala Gln Ala Thr Glu Thr Val	980	985	990	2976
GGG GAC TGG ACG AGA TCA GCA GTG TAG CCC GTG GGA CGC AAG GCT TCC Gly Asp Trp Thr Arg Ser Ala Val * Pro Val Gly Arg Lys Ala Ser	995	1000	1005	3024
CGG GAC CCT GCA CCT GGA GAC GGA TCT CCA GTC TGG AGT CAG AAG TGT Arg Asp Pro Ala Pro Gly Asp Gly Ser Pro Val Trp Ser Gln Lys Cys	1010	1015	1020	3072
GAG TTA TCA GCC ACT CAG GCT CCG AGC CAG CTG GAT TCT CTG CCT GCC Glu Leu Ser Ala Thr Gln Ala Pro Ser Gln Leu Asp Ser Leu Pro Ala	1025	1030	1035	3120
ACT GTC AGG GTT AAG CGG CAG GCA GGA TTG GCC CTT CTC TGG CTT CTA Thr Val Arg Val Lys Arg Gln Ala Gly Leu Ala Leu Leu Trp Leu Leu	1045	1050	1055	3168
CCA TGA AAT CCT GGC CAT GGC ACC CCA GTG ACA GAT GAT GTC TTC CAT Pro * Asn Pro Gly His Gly Thr Pro Val Thr Asp Asp Val Phe His	1060	1065	1070	3216
GGT CAT CAG TGA CCT CAG CTA GCC TCA Gly His Gln * Pro Gln Leu Ala Ser	1075	1080		3243

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4092 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both

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(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 189..3923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	230
1                       5                       10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15                     20                     25                     30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35                     40                     45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50                     55                     60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65                     70                     75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80                     85                     90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95                     100                     105                     110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115                     120                     125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	614
130                     135                     140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	662
145                     150                     155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	710
160                     165                     170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	758
175                     180                     185                     190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA	806

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Val	Ser	Trp	Arg	Leu	Leu	Asp	Val	Val	Thr	Leu	Glu	Leu	Asp	Pro	Gly	
				195					200					205		
GGG	CCG	CGC	GCG	CGC	ACG	CAG	CGC	CTG	CTG	CGC	CAG	CTC	GAC	GCG	CCC	
Gly	Pro	Arg	Ala	Arg	Thr	Gln	Arg	Leu	Leu	Arg	Gln	Leu	Asp	Ala	Pro	
				210					215					220		
GTG	TTT	GTG	GCC	TAC	TGC	TCG	CGC	GAG	GAG	GCC	GAG	GTG	CTC	TTC	GCC	
Val	Phe	Val	Ala	Tyr	Cys	Ser	Arg	Glu	Glu	Ala	Glu	Val	Leu	Phe	Ala	
				225				230				235			902	
GAG	GCG	GCG	CAG	GCC	GGT	CTG	GTG	GGG	CCC	GGC	CAC	GTG	TGG	CTG	GTG	
Glu	Ala	Ala	Gln	Ala	Gly	Leu	Val	Gly	Pro	Gly	His	Val	Trp	Leu	Val	
				240			245				250				950	
CCC	AAC	CTG	GCG	CTG	GGC	AGC	ACC	GAT	GCG	CCC	CCC	GCC	ACC	TTC	CCC	
Pro	Asn	Leu	Ala	Leu	Gly	Ser	Thr	Asp	Ala	Pro	Pro	Ala	Thr	Phe	Pro	
				255			260				265				998	
GTG	GGC	CTC	ATC	AGC	GTC	GTC	ACC	GAG	AGC	TGG	CGC	CTC	AGC	CTG	CGC	
Val	Gly	Leu	Ile	Ser	Val	Val	Thr	Glu	Ser	Trp	Arg	Leu	Ser	Leu	Arg	
				275				280						285	1046	
CAG	AAG	GTG	CGC	GAC	GGC	GTG	GCC	ATT	CTG	GCC	CTG	GGC	GCC	CAC	AGC	
Gln	Lys	Val	Arg	Asp	Gly	Val	Ala	Ile	Leu	Ala	Leu	Gly	Ala	His	Ser	
				290				295						300	1094	
TAC	TGG	CGC	CAG	CAT	GGA	ACC	CTG	CCA	GCC	CCG	GCC	GGG	GAC	TGC	CGT	
Tyr	Trp	Arg	Gln	His	Gly	Thr	Leu	Pro	Ala	Pro	Ala	Gly	Asp	Cys	Arg	
				305			310							315	1142	
GTT	CAC	CCT	GGG	CCC	GTC	AGC	CCT	GCC	CGG	GAG	GCC	TTC	TAC	AGG	CAC	
Val	His	Pro	Gly	Pro	Val	Ser	Pro	Ala	Arg	Glu	Ala	Phe	Tyr	Arg	His	
				320			325							330	1190	
CTA	CTG	AAT	GTC	ACC	TGG	GAG	GGC	CGA	GAC	TTC	TCC	TTC	AGC	CCT	GGT	
Leu	Leu	Asn	Val	Thr	Trp	Glu	Gly	Arg	Asp	Phe	Ser	Phe	Ser	Pro	Gly	
				335			340				345				350	1238
GGG	TAC	CTG	GTC	CAG	CCC	ACC	ATG	GTG	GTG	ATC	GCC	CTC	AAC	CGG	CAC	
Gly	Tyr	Leu	Val	Gln	Pro	Thr	Met	Val	Val	Ile	Ala	Leu	Asn	Arg	His	
				355				360						365	1286	
CGC	CTC	TGG	GAG	ATG	GTG	GGG	CGC	TGG	GAG	CAT	GGC	GTC	CTA	TAC	ATG	
Arg	Leu	Trp	Glu	Met	Val	Gly	Arg	Trp	Glu	His	Gly	Val	Leu	Tyr	Met	
				370			375							380	1334	
AAG	TAC	CCC	GTG	TGG	CCT	CGC	TAC	AGT	GCC	TCT	CTG	CAG	CCT	GTG	GTG	
Lys	Tyr	Pro	Val	Trp	Pro	Arg	Tyr	Ser	Ala	Ser	Leu	Gln	Pro	Val	Val	
				385			390				395				1382	
GAC	AGT	CGG	CAC	CTG	ACG	GTG	GCC	ACG	CTG	GAA	GAG	CGG	CCC	TTT	GTC	
Asp	Ser	Arg	His	Leu	Thr	Val	Ala	Thr	Leu	Glu	Glu	Arg	Pro	Phe	Val	
				400			405							410	1430	
ATC	GTG	GAG	AGC	CCT	GAC	CCT	GGC	ACA	GGA	GGC	TGT	GTC	CCC	AAC	ACC	
Ile	Val	Glu	Ser	Pro	Asp	Pro	Gly	Thr	Gly	Gly	Cys	Val	Pro	Asn	Thr	
				415			420				425				430	1478
GTG	CCC	TGC	CGC	AGG	CAG	AGC	AAC	CAC	ACC	TTC	AGC	AGC	GGG	GAC	GTG	
Val	Pro	Cys	Arg	Arg	Gln	Ser	Asn	His	Thr	Phe	Ser	Ser	Gly	Asp	Val	
				435				440						445	1526	
GCC	CCC	TAC	ACC	AAG	CTC	TGC	TGT	AAG	GGA	TTC	TGC	ATC	GAC	ATC	CTC	
Ala	Pro	Tyr	Thr	Lys	Leu	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile	Leu	
				450			455							460	1574	

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AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val 465 470 475	1622
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met 480 485 490	1670
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu 495 500 505 510	1718
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe 515 520 525	1766
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val 530 535 540	1814
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG Ser Pro Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met 545 550 555	1862
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe 560 565 570	1910
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
AAG TCC GGG GGC CCA GCT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu 595 600 605	2006
TGG GCG CTG GTC TTC AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly 610 615 620	2054
ACC ACC AGC AAG ATC ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile 625 630 635	2102
TTC CTC GCC AGA TAC ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu 640 645 650	2150
CAA TAC ATC GAC ACT GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg 655 660 665 670	2198
CCT CAA GAT CAG TAC CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly 675 680 685	2246
AGC ACG GAG CGG AAC ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His 690 695 700	2294
ATG GTC AAG TTC AAC CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu 705 710 715	2342
AAG ATG GGC TCT GAG GCT CAG CCT GTC CCC AGG AAG CTG GAT GCC TTC Lys Met Gly Ser Glu Ala Gln Pro Val Pro Arg Lys Leu Asp Ala Phe 720 725 730	2390

ATC TAT GAT GCT GCT GTC CTC AAC TAC ATG GCA GGC AAG GAC GAG GGC Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys Asp Glu Gly 735 740 745 750	2438
TGC AAG CTG GTC ACC ATT GGG TCT GGC AAG GTC TTT GCT ACC ACT GGC Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly 755 760 765	2486
TAC GGC ATC GCC ATG CAG AAG GAC TCC CAC TGG AAG CGG GCC ATA GAC Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp 770 775 780	2534
CTG GCG CTC TTG CAG TTC CTG GGG GAC GGA GAG ACA CAG AAA CTG GAG Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu 785 790 795	2582
ACA GTG TGG CTC TCA GGG ATC TGC CAG AAT GAG AAG AAC GAG GTG ATG Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met 800 805 810	2630
AGC AGC AAG CTG GAC ATC GAC AAC ATG GGA GGC GTC TTC TAC ATG CTG Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu 815 820 825 830	2678
CTG GTG GCC ATG GGG CTG GCC CTG CTG GTC TTC GCC TGG GAG CAC CTG Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu 835 840 845	2726
GTC TAC TGG AAG CTG CGC CAC TCG GTG CCC AAC TCA TCC CAG CTG GAC Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp 850 855 860	2774
TTC CTG CTG GCT TTC AGC AGG GGC ATC TAC AGC TGC TTC AGC GGG GTG Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val 865 870 875	2822
CAG AGC CTC GCC AGC CCA CCG CGG CAG GCC AGC CCG GAC CTC ACG GCC Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala 880 885 890	2870
AGC TCG GCC CAG GCC AGC GTG CTC AAG ATT CTG CAG GCA GCC CGC GAC Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp 895 900 905 910	2918
ATG GTG ACC ACG GCG GGC GTA AGC AAC TCC CTG GAC CGC GCC ACT CGC Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg 915 920 925	2966
ACC ATC GAG AAT TGG GGT GGC GGC CGC CGT GCG CCC CCA CCG TCC CCC Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro 930 935 940	3014
TGC CCG ACC CCG CGG TCT GGC CCC AGC CCA TGC CTG CCC ACC CCC GAC Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp 945 950 955	3062
CCG CCC CCA GAG CCG AGC CCC ACG GGC TGG GGA CCG CCA GAC GGG GGT Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly GLY 960 965 970	3110
CGC GCG GCG CTT GTG CGC AGG GCT CCG CAG CCC CCG GGC CGC CCC CCG Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro 975 980 985 990	3158
ACG CCG GGG CCG CCC CTG TCC GAC GTC TCC CGA GTG TCG CGC CGC CCA Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro 995 1000 1005	3206

GCC TGG GAG GCG CGG TGG CCG GTG CGG ACC GGG CAC TGC GGG AGG CAC Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His 1010 1015 1020	3254
CTC TCG GCC TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT CAC TAC AGC Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser 1025 1030 1035	3302
TCC TTT CCT CGA GCC GAC CGA TCC GGC CGC CCC TTC CTC CCG CTC TTC Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe 1040 1045 1050	3350
CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT CCG GAG CAG Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln 1055 1060 1065 1070	3398
CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC CGG GGC TCG Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser 1075 1080 1085	3446
CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG GCC TTC GCT Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala 1090 1095 1100	3494
CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC TGC GCC CGC Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg 1105 1110 1115	3542
CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG CAG TCG ATG Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met 1120 1125 1130	3590
TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG CAG GCA GGG Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly 1135 1140 1145 1150	3638
GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC GCC CAC GCC Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala 1155 1160 1165	3686
CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT CCA CCC TGT His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys 1170 1175 1180	3734
GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT CTG GGG CAC Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His 1185 1190 1195	3782
AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC AGT GGG GGA Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly 1200 1205 1210	3830
CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC TTC CCG GGA Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly 1215 1220 1225 1230	3878
CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA GTG TGAGTTATCA Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val 1235 1240 124	3930
GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCCTGCCA CTGTCAGGGT TAAGCGGCAG	3990
GCAGGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA	4050
GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4092

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1244 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly  
1 5 10 15

Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val  
20 25 30

Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val  
35 40 45

Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro  
50 55 60

Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln  
65 70 75 80

Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu  
85 90 95

Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser  
100 105 110

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val  
115 120 125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val  
130 135 140

Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr  
145 150 155 160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala  
165 170 175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser  
180 185 190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro  
195 200 205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe  
210 215 220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala  
225 230 235 240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn  
245 250 255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly  
260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys  
275 280 285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp

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290

295

300

Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His			
305	310	315	320
Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu			
325	330	335	
Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr			
340	345	350	
Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu			
355	360	365	
Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr			
370	375	380	
Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser			
385	390	395	400
Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val			
405	410	415	
Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro			
420	425	430	
Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro			
435	440	445	
Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys			
450	455	460	
Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn			
465	470	475	480
Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly			
485	490	495	
Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile			
500	505	510	
Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu			
515	520	525	
Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro			
530	535	540	
Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe			
545	550	555	560
Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr			
565	570	575	
Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser			
580	585	590	
Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala			
595	600	605	
Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr			
610	615	620	
Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu			
625	630	635	640
Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr			

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645

650

655

Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln  
660 665 670

Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr  
675 680 685

Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val  
690 695 700

Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met  
705 710 715 720

Gly Ser Glu Ala Gln Pro Val Pro Arg Lys Leu Asp Ala Phe Ile Tyr  
725 730 735

Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys  
740 745 750

Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly  
755 760 765

Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala  
770 775 780

Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val  
785 790 795 800

Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser  
805 810 815

Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val  
820 825 830

Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu Val Tyr  
835 840 845

Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu  
850 855 860

Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser  
865 870 875 880

Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser  
885 890 895

Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val  
900 905 910

Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile  
915 920 925

Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro  
930 935 940

Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro  
945 950 955 960

Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala  
965 970 975

Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro  
980 985 990

Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp

995	1000	1005
Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His Leu Ser		
1010	1015	1020
Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe		
1025	1030	1035
1040		
Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu		
1045	1050	1055
Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala		
1060	1065	1070
Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro		
1075	1080	1085
Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro		
1090	1095	1100
Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp		
1105	1110	1115
1120		
Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu		
1125	1130	1135
Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro		
1140	1145	1150
Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala His Leu		
1155	1160	1165
Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser		
1170	1175	1180
His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly		
1185	1190	1195
1200		
Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp		
1205	1210	1215
Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys		
1220	1225	1230
Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val		
1235	1240	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 189..3884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCTTGA GCCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATGCCCG GCCTAAAAAT ACCCGAACT TCACAGCCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	230
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	614
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	662
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	710
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	758
175 180 185 190	
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	806
195 200 205	
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	854
210 215 220	
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala	902
225 230 235	

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GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val 240 245 250	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro 255 260 265 270	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg 275 280 285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser 290 295 300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg 305 310 315	1142
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His 320 325 330	1190
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly 335 340 345 350	1238
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His 355 360 365	1286
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met 370 375 380	1334
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val 385 390 395	1382
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Arg Pro Phe Val 400 405 410	1430
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr 415 420 425 430	1478
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val 435 440 445	1526
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu 450 455 460	1574
AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val 465 470 475	1622
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met 480 485 490	1670
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu 495 500 505 510	1718

ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe 515 520 525	1766
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val 530 535 540	1814
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met 545 550 555	1862
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe 560 565 570	1910
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
ACT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG TGG GCG CTG GTC TTC Thr Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe 595 600 605	2006
AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC ACC ACC AGC AAG ATC Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile 610 615 620	2054
ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC TTC CTC GCC AGA TAC Met Val Leu Val Trp Ala Phe Ala Val Ile Phe Leu Ala Arg Tyr 625 630 635	2102
ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG CAA TAC ATC GAC ACT Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr 640 645 650	2150
GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG CCT CAA GAT CAG TAC Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr 655 660 665 670	2198
CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC AGC ACG GAG CGG AAC Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn 675 680 685	2246
ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC ATG GTC AAG TTC AAC Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn 690 695 700	2294
CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC AAG ATG GGG AAG CTG Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Leu 705 710 715	2342
GAT GCC TTC ATC TAT GAT GCT GCT GTC CTC AAC TAC ATG GCA GGC AAG Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys 720 725 730	2390
GAC GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT GGC AAG GTC TTT GCT Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala 735 740 745 750	2438
ACC ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC TCC CAC TGG AAG CGG Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg 755 760 765	2486
GCC ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG GAC GGA GAG ACA CAG Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln 770 775 780	2534

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AAA CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC CAG AAT GAG AAG AAC Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn 785 790 795	2582
GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG GGA GGC GTC TTC Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe 800 805 810	2630
TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG CTG GTC TTC GCC TGG Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp 815 820 825 830	2678
GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG GTG CCC AAC TCA TCC Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser 835 840 845	2726
CAG CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC ATC TAC AGC TGC TTC Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe 850 855 860	2774
AGC GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG CAG GCC AGC CCG GAC Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp 865 870 875	2822
CTC ACG GCC AGC TCG GCC CAG GCC AGC GTG CTC AAG ATT CTG CAG GCA Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala 880 885 890	2870
GCC CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC AAC TCC CTG GAC CGC Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg 895 900 905 910	2918
GCC ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC CGC CGT GCG CCC CCA Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro 915 920 925	2966
CCG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC AGC CCA TGC CTG CCC Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro 930 935 940	3014
ACC CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG GGC TGG GGA CCG CCA Thr Pro Asp Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro 945 950 955	3062
GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT CCG CAG CCC CCG GGC Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly 960 965 970	3110
CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC GTC TCC CGA GTG TCG Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser 975 980 985 990	3158
CGC CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG CGG ACC GGG CAC TGC Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys 995 1000 1005	3206
GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys 1010 1015 1020	3254
CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC GGC CGC CCC TTC CTC His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu 1025 1030 1035	3302
CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly 1040 1045 1050	3350

CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala	3398
1055 1060 1065 1070	
CGG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu	3446
1075 1080 1085	
GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala	3494
1090 1095 1100	
TGC GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala	3542
1105 1110 1115	
CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC TGC CAG GAG GGC GAG Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu	3590
1120 1125 1130	
CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His	3638
1135 1140 1145 1150	
GCC CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu	3686
1155 1160 1165	
CCA CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro	3734
1170 1175 1180	
CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp	3782
1185 1190 1195	
AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly	3830
1200 1205 1210	
TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu	3878
1215 1220 1225 1230	
GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA Val	3931
CA	4053

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1231 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly

1	5	10	15
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val			
20	25		30
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val			
35	40		45
Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro			
50	55		60
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln			
65	70	75	80
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu			
85	90		95
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser			
100	105		110
Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val			
115	120	125	
Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val			
130	135		140
Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr			
145	150	155	160
Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala			
165	170		175
Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser			
180	185		190
Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro			
195	200	205	
Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe			
210	215		220
Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala			
225	230	235	240
Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn			
245	250		255
Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly			
260	265		270
Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys			
275	280		285
Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp			
290	295		300
Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His			
305	310	315	320
Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu			
325	330		335
Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr			
340	345		350
Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu			

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355	360	365
Trp Glu Met Val Gly Arg	Trp Glu His Gly Val	Leu Tyr Met Lys Tyr
370	375	380
Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln	Pro Val Val Asp Ser	
385	390	395 400
Arg His Leu Thr Val Ala Thr Leu Glu	Glu Arg Pro Phe Val Ile Val	
405	410	415
Glu Ser Pro Asp Pro Gly Thr Gly	Cys Val Pro Asn Thr Val Pro	
420	425	430
Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly	Asp Val Ala Pro	
435	440	445
Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp	Ile Leu Lys Lys	
450	455	460
Leu Ala Arg Val Val Lys Phe Ser Tyr Asp	Leu Tyr Leu Val Thr Asn	
465	470	475 480
Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly	Met Ile Gly	
485	490	495
Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser	Leu Thr Ile	
500	505	510
Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro	Phe Val Glu	
515	520	525
Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly	Thr Val Ser Pro	
530	535	540
Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met	Met Phe	
545	550	555 560
Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met	Phe Glu Tyr	
565	570	575
Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly	Lys Thr Phe	
580	585	590
Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val	Phe Asn Asn	
595	600	605
Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys	Ile Met Val	
610	615	620
Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg	Tyr Thr Ala	
625	630	635 640
Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp	Thr Val Ser	
645	650	655
Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln	Tyr Pro Pro	
660	665	670
Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg	Asn Ile Arg	
675	680	685
Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys	Phe Asn Gln Arg	
690	695	700
Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys	Leu Asp Ala	

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705	710	715	720
Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Lys Asp Glu			
725	730	735	
Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr			
740	745	750	
Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile			
755	760	765	
Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu			
770	775	780	
Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val			
785	790	795	800
Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met			
805	810	815	
Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His			
820	825	830	
Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu			
835	840	845	
Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly			
850	855	860	
Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr			
865	870	875	880
Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg			
885	890	895	
Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr			
900	905	910	
Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser			
915	920	925	
Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro			
930	935	940	
Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly			
945	950	955	960
Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro			
965	970	975	
Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg			
980	985	990	
Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg			
995	1000	1005	
His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr			
1010	1015	1020	
Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu			
1025	1030	1035	1040
Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu			
1045	1050	1055	
Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly			

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1060

1065

1070

Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe  
 1075 1080 1085  
 Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala  
 1090 1095 1100  
 Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser  
 1105 1110 1115 1120  
 Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala  
 1125 1130 1135  
 Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His  
 1140 1145 1150  
 Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro  
 1155 1160 1165  
 Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly  
 1170 1175 1180  
 His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly  
 1185 1190 1195 1200  
 Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro  
 1205 1210 1215  
 Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val  
 1220 1225 1230

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 4017 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
      (A) NAME/KEY: CDS  
      (B) LOCATION: 189..3848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA GCGCGGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCCG AGTGACCCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1                 5                 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15                 20                 25                 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	

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	35	40	45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	50	55	60	374
CAG CCG CTC ACA GTT GGG GTC AAC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	65	70	75	422
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	80	85	90	470
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	95	100	105	518
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	115	120	125	566
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	130	135	140	614
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	145	150	155	662
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	160	165	170	710
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	175	180	185	758
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly	195	200	205	806
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro	210	215	220	854
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala	225	230	235	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val	240	245	250	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro	255	260	265	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg	275	280	285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser	290	295	300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT				1142

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Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg		
305 310 315		
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC		1190
Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His		
320 325 330		
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT		1238
Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly		
335 340 345 350		
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC		1286
Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His		
355 360 365		
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG		1334
Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met		
370 375 380		
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG		1382
Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val		
385 390 395		
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC		1430
Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val		
400 405 410		
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC		1478
Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr		
415 420 425 430		
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG		1526
Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val		
435 440 445		
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC		1574
Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu		
450 455 460		
AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG		1622
Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val		
465 470 475		
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG		1670
Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met		
480 485 490		
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC		1718
Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu		
495 500 505 510		
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT		1766
Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe		
515 520 525		
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC		1814
Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val		
530 535 540		
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG		1862
Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met		
545 550 555		
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC		1910
Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe		
560 565 570		

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GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
AAG TCC GGG GGC CCA GCT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG Lys Ser Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu 595 600 605	2006
TGG GCG CTG GTC TTC AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC Trp Ala Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly 610 615 620	2054
ACC ACC AGC AAG ATC ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC Thr Thr Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile 625 630 635	2102
TTC CTC GCC AGA TAC ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG Phe Leu Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu 640 645 650	2150
CAA TAC ATC GAC ACT GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG Gln Tyr Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg 655 660 665 670	2198
CCT CAA GAT CAG TAC CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC Pro Gln Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly 675 680 685	2246
AGC ACG GAG CGG AAC ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC Ser Thr Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His 690 695 700	2294
ATG GTC AAG TTC AAC CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC Met Val Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu 705 710 715	2342
AAG ATG GGC AAG GAC GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT GGC Lys Met Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly 720 725 730	2390
AAG GTC TTT GCT ACC ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC TCC Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser 735 740 745 750	2438
CAC TGG AAG CGG GCC ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG GAC His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp 755 760 765	2486
GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC CAG Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln 770 775 780	2534
AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met 785 790 795	2582
GGA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG CTG Gly Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu 800 805 810	2630
GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG GTG Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val 815 820 825 830	2678
CCC AAC TCA TCC CAG CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC ATC Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile 835 840 845	2726

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TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG CAG Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln 850 855 860	2774
GCC AGC CCG GAC CTC ACG GCC AGC TCG GCC CAG GGC AGC GTG CTC AAG Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys 865 870 875	2822
ATT CTG CAG GCA GCC CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC AAC Ile Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn 880 885 890	2870
TCC CTG GAC CGC GCC ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC CGC Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Gly Arg 895 900 905 910	2918
CGT GCG CCC CCA CCG TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC AGC Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser 915 920 925	2966
CCA TGC CTG CCC ACC CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG GGC Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly 930 935 940	3014
TGG GGA CCG CCA GAC GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT CCG Trp Gly Pro Pro Asp Gly Arg Ala Ala Leu Val Arg Arg Ala Pro 945 950 955	3062
CAG CCC CCG GGC CGC CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC GTC Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val 960 965 970	3110
TCC CGA GTG TCG CGC CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG CGG Ser Arg Val Ser Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg 975 980 985 990	3158
ACC GGG CAC TGC GGG AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG TCG Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser 995 1000 1005	3206
CCC GCG CGC TGT CAC TAC AGC TCC TTT CCT CGA GCC GAC CGA TCC GGC Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly 1010 1015 1020	3254
CGC CCC TTC CTC CCG CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC CTG Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu 1025 1030 1035	3302
CCG CTG CTC GGT CCG GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn 1040 1045 1050	3350
GCG GCC TGG GCC CGG GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser 1055 1060 1065 1070	3398
TCC GTG GCC GAG GCC TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys 1075 1080 1085	3446
ACC GGC CCC GCC TGC GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg 1090 1095 1100	3494
TTG GCG CAG GCG CAG TCG ATG TGC TTG CCG ATC TAC CGG GAG GCC TGC Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys 1105 1110 1115	3542

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CAG GAG GGC GAG CAG GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His 1120 1125 1130	3590
GTC TGC CTG CAC GCC CAC CTC CCA TTG TGC TGG GGG GCT GTC Val Cys Leu His Ala His Leu Pro Leu Cys Trp Gly Ala Val 1135 1140 1145 1150	3638
TGT CCT CAC CTT CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly 1155 1160 1165	3686
GCC TGG GGG CCT CTG GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr 1170 1175 1180	3734
GGC TAC AGA GAC AGT GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg 1185 1190 1195	3782
GGG ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser 1200 1205 1210	3830
CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT Leu Glu Ser Glu Val 122	3885
CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA	3945
TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4005
	4017

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1219 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly 1 5 10 15	
Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val 20 25 30	
Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val 35 40 45	
Arg. Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro 50 55 60	
Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln 65 70 75 80	
Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu 85 90 95	
Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser 100 105 110	

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val  
115 120 125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val  
130 135 140

Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr  
145 150 155 160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala  
165 170 175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser  
180 185 190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro  
195 200 205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe  
210 215 220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala  
225 230 235 240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn  
245 250 255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly  
260 265 270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys  
275 280 285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp  
290 295 300

Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His  
305 310 315 320

Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu  
325 330 335

Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr  
340 345 350

Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu  
355 360 365

Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr  
370 375 380

Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser  
385 390 395 400

Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val  
405 410 415

Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro  
420 425 430

Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro  
435 440 445

Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys  
450 455 460

Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn

465                  470                  475                  480  
Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly  
485                  490                  495  
Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile  
500                  505                  510  
Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu  
515                  520                  525  
Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro  
530                  535                  540  
Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe  
545                  550                  555                  560  
Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr  
565                  570                  575  
Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Lys Ser  
580                  585                  590  
Gly Gly Pro Ala Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala  
595                  600                  605  
Leu Val Phe Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr  
610                  615                  620  
Ser Lys Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu  
625                  630                  635                  640  
Ala Arg Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr  
645                  650                  655  
  
Ile Asp Thr Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln  
660                  665                  670  
Asp Gln Tyr Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr  
675                  680                  685  
Glu Arg Asn Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val  
690                  695                  700  
Lys Phe Asn Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met  
705                  710                  715                  720  
Gly Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val  
725                  730                  735  
Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp  
740                  745                  750  
Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu  
755                  760                  765  
Thr Gln Lys Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu  
770                  775                  780  
Lys Asn Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly  
785                  790                  795                  800  
Val Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe  
805                  810                  815  
Ala Trp Glu His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn

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820	825	830
Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser		
835	840	845
Cys Phe Ser Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser		
850	855	860
Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu		
865	870	875
Gln Ala Ala Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu		
885	890	895
Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala		
900	905	910
Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys		
915	920	925
Leu Pro Thr Pro Asp Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly		
930	935	940
Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro		
945	950	955
960		
Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg		
965	970	975
Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly		
980	985	990
His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala		
995	1000	1005
Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro		
1010	1015	1020
Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu		
1025	1030	1035
1040		
Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala		
1045	1050	1055
Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val		
1060	1065	1070
Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly		
1075	1080	1085
Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala		
1090	1095	1100
Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu		
1105	1110	1115
1120		
Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys		
1125	1130	1135
Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro		
1140	1145	1150
His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp		
1155	1160	1165
Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr		

1170                    1175                    1180  
Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr  
1185                    1190                    1195                    1200  
Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu  
1205                    1210                    1215  
Ser Glu Val

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4077 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 189..3908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CCCTTAATAA GATTTCACNAC GTACACTCGA GCCATCGCGA GTGTCTTGA GCGCGGGTG	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT GCCACGTTCC	120
CTATGAATTA TTTATCGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCCG AGTGACCCTC	180
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	230
1                5                    10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	278
15              20                    25                    30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC Thr Val Ala Val Val Phe Ser Ser Gly Pro Pro Gln Ala Gln Phe	326
35              40                    45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	374
50              55                    60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	422
65              70                    75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	470
80              85                    90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	518
95              100                   105                   110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	566
115             120                   125	

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GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu 130 135 140	614
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu 145 150 155	662
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly 160 165 170	710
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His 175 180 185 190	758
GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly 195 200 205	806
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro 210 215 220	854
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala 225 230 235	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val 240 245 250	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro 255 260 265 270	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg 275 280 285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser 290 295 300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg 305 310 315	1142
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His 320 325 330	1190
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly 335 340 345 350	1238
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His 355 360 365	1286
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met 370 375 380	1334
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val 385 390 395	1382

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GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val 400 405 410	1430
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr 415 420 425 430	1478
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val 435 440 445	1526
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu 450 455 460	1574
AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val 465 470 475	1622
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met 480 485 490	1670
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu 495 500 505 510	1718
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe 515 520 525	1766
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val 530 535 540	1814
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG Ser Pro Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met 545 550 555	1862
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe 560 565 570	1910
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
ACT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG TGG GCG CTG GTC TTC Thr Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe 595 600 605	2006
AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC ACC ACC AGC AAG ATC Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile 610 615 620	2054
ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC TTC CTC GCC AGA TAC Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr 625 630 635	2102
ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG CAA TAC ATC GAC ACT Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr 640 645 650	2150
GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG CCT CAA GAT CAG TAC Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr 655 660 665 670	2198

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CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC AGC ACG GAG CGG AAC Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn 675 680 685	2246
ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC ATG GTC AAG TTC AAC Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn 690 695 700	2294
CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC AAG ATG GGC TCT GAG Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Ser Glu 705 710 715	2342
GCT CAG CCT GTC CCC AGG AAG CTG GAT GCC TTC ATC TAT GAT GCT GCT Ala Gln Pro Val Pro Arg Lys Leu Asp Ala Phe Ile Tyr Asp Ala Ala 720 725 730	2390
GTC CTC AAC TAC ATG GCA GGC AAG GAC GAG GGC TGC AAG CTG GTC ACC Val Leu Asn Tyr Met Ala Gly Lys Asp Glu Gly Cys Lys Leu Val Thr 735 740 745 750	2438
ATT GGG TCT GGC AAG GTC TTT GCT ACC ACT GGC TAC GGC ATC GCC ATG Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly Tyr Gly Ile Ala Met 755 760 765	2486
CAG AAG GAC TCC CAC TGG AAG CGG GCC ATA GAC CTG GCG CTC TTG CAG Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp Leu Ala Leu Leu Gln 770 775 780	2534
TTC CTG GGG GAC GGA GAG ACA CAG AAA CTG GAG ACA GTG TGG CTC TCA Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu Thr Val Trp Leu Ser 785 790 795	2582
GGG ATC TGC CAG AAT GAG AAG AAC GAG GTG ATG AGC AGC AAG CTG GAC Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met Ser Ser Lys Leu Asp 800 805 810	2630
ATC GAC AAC ATG GGA GGC GTC TTC TAC ATG CTG CTG GTG GCC ATG GGG Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu Leu Val Ala Met Gly 815 820 825 830	2678
CTG GCC CTG CTG GTC TTC GCC TGG GAG CAC CTG GTC TAC TGG AAG CTG Leu Ala Leu Val Phe Ala Trp Glu His Leu Val Tyr Trp Lys Leu 835 840 845	2726
CGC CAC TCG GTG CCC AAC TCA TCC CAG CTG GAC TTC CTG CTG GCT TTC Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp Phe Leu Leu Ala Phe 850 855 860	2774
AGC AGG GGC ATC TAC AGC TGC TTC AGC GGG GTG CAG AGC CTC GCC AGC Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val Gln Ser Leu Ala Ser 865 870 875	2822
CCA CCG CGG CAG GCC AGC CCG GAC CTC ACG GCC AGC TCG GCC CAG GCC Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala Ser Ser Ala Gln Ala 880 885 890	2870
AGC GTG CTC AAG ATT CTG CAG GCA GCC CGC GAC ATG GTG ACC ACG GCG Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp Met Val Thr Thr Ala 895 900 905 910	2918
GGC GTA AGC AAC TCC CTG GAC CGC GCC ACT CGC ACC ATC GAG AAT TGG Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg Thr Ile Glu Asn Trp 915 920 925	2966
GGT GGC GGC CGC CGT GCG CCC CCA CCG TCC CCC TGC CCG ACC CCG CGG Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg 930 935 940	3014

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TCT	GGC	CCC	AGC	CCA	TGC	CTG	CCC	ACC	CCC	GAC	CCG	CCC	CCA	GAG	CCG		3062
Ser	Gly	Pro	Ser	Pro	Cys	Leu	Pro	Thr	Pro	Asp	Pro	Pro	Pro	Pro	Glu	Pro	
945							950							955			
AGC	CCC	ACG	GGC	TGG	GGA	CCG	CCA	GAC	GGG	GGT	CGC	GCG	GCG	CTT	GTG		3110
Ser	Pro	Thr	Gly	Trp	Gly	Pro	Pro	Asp	Gly	Gly	Arg	Ala	Ala	Leu	Val		
960						965					970						
CGC	AGG	GCT	CCG	CAG	CCC	CCG	GGC	CGC	CCC	CCG	ACG	CCG	GGG	CCG	CCC		3158
Arg	Arg	Ala	Pro	Gln	Pro	Pro	Gly	Arg	Pro	Pro	Thr	Pro	Gly	Pro	Pro		
975							980				985			990			
CTG	TCC	GAC	GTC	TCC	CGA	GTG	TCG	CGC	CGC	CCA	GCC	TGG	GAG	GCG	CGG		3206
Leu	Ser	Asp	Val	Ser	Arg	Val	Ser	Arg	Arg	Pro	Ala	Trp	Glu	Ala	Arg		
995								1000					1005				
TGG	CCG	GTG	CGG	ACC	GGG	CAC	TGC	GGG	AGG	CAC	CTC	TCG	GCC	TCC	GAG		3254
Trp	Pro	Val	Arg	Thr	Gly	His	Cys	Gly	Arg	His	Leu	Ser	Ala	Ser	Glu		
1010							1015						1020				
CGG	CCC	CTG	TCG	CCC	GCG	CGC	TGT	CAC	TAC	AGC	TCC	TTT	CCT	CGA	GCC		3302
Arg	Pro	Leu	Ser	Pro	Ala	Arg	Cys	His	Tyr	Ser	Ser	Phe	Pro	Arg	Ala		
1025							1030					1035					
GAC	CGA	TCC	GGC	CGC	CCC	TTC	CTC	CCG	CTC	TTC	CCG	GAG	CCC	CCG	GAG		3350
Asp	Arg	Ser	Gly	Arg	Pro	Phe	Leu	Pro	Leu	Phe	Pro	Glu	Pro	Pro	Glu		
1040							1045					1050					
CTG	GAG	GAC	CTG	CCG	CTG	CTC	GGT	CCG	GAG	CAG	CTG	GCC	CGG	CGG	GAG		3398
Leu	Glu	Asp	Leu	Pro	Leu	Leu	Gly	Pro	Glu	Gln	Leu	Ala	Arg	Arg	Glu		
1055							1060				1065			1070			
GCC	CTG	CTG	AAC	GCG	GCC	TGG	GCC	CGG	GGC	TCG	CGC	CCG	AGT	CAC	GCT		3446
Ala	Leu	Leu	Asn	Ala	Ala	Trp	Ala	Arg	Gly	Ser	Arg	Pro	Ser	His	Ala		
1075								1080					1085				
TCC	CTG	CCC	AGC	TCC	GTG	GCC	GAG	GCC	TTC	GCT	CGG	CCC	AGC	TCG	CTG		3494
Ser	Leu	Pro	Ser	Ser	Val	Ala	Glu	Ala	Phe	Ala	Arg	Pro	Ser	Ser	Leu		
1090							1095						1100				
CCC	GCT	GGG	TGC	ACC	GGC	CCC	GCC	TGC	GCC	CGC	CCC	GAC	GGC	CAC	TCG		3542
Pro	Ala	Gly	Cys	Thr	Gly	Pro	Ala	Cys	Ala	Arg	Pro	Asp	Gly	His	Ser		
1105							1110					1115					
GCC	TGC	AGG	CGC	TTG	GCG	CAG	GCG	CAG	TCG	ATG	TGC	TTG	CCG	ATC	TAC		3590
Ala	Cys	Arg	Arg	Leu	Ala	Gln	Ala	Gln	Ser	Met	Cys	Leu	Pro	Ile	Tyr		
1120							1125					1130					
CGG	GAG	GCC	TGC	CAG	GAG	GGC	GAG	CAG	GCA	GGG	GCC	CCC	GCC	TGG	CAG		3638
Arg	Glu	Ala	Cys	Gln	Glu	Gly	Glu	Gln	Ala	Gly	Ala	Pro	Ala	Trp	Gln		
1135							1140				1145			1150			
CAC	AGA	CAG	CAC	GTC	CTG	CAC	GCC	CAC	GCC	CAC	CTG	CCA	TTG	TGC		3686	
His	Arg	Gln	His	Val	Cys	Leu	His	Ala	His	Ala	His	Leu	Pro	Leu	Cys		
1155							1160				1165						
TGG	GGG	GCT	GTC	TGT	CCT	CAC	CTT	CCA	CCC	TGT	GAC	AGC	CAC	GGC	TCC		3734
Trp	Gly	Ala	Val	Cys	Pro	His	Leu	Pro	Pro	Cys	Asp	Ser	His	Gly	Ser		
1170							1175					1180					
TGG	CTC	TCC	GCG	GCC	TGG	GGG	CCT	CTG	GGG	CAC	AGC	GGC	AGG	ACT	CTG		3782
Trp	Leu	Ser	Gly	Ala	Trp	Gly	Pro	Leu	Gly	His	Ser	Gly	Arg	Thr	Leu		
1185							1190					1195					
GGG	CTG	GGC	ACA	GGC	TAC	AGA	GAC	AGT	GGG	GGA	CTG	GAC	GAG	ATC	AGC		3830
Gly	Leu	Gly	Thr	Gly	Tyr	Arg	Asp	Ser	Gly	Gly	Leu	Asp	Glu	Ile	Ser		
1200							1205					1210					

AGT GTA GCC CGT GGC ACG CAA GGC TTC CCG GGA CCC TGC ACC TGG AGA	3878
Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg	
1215 1220 1225 1230	
CGG ATC TCC AGT CTG GAG TCA GAA GTG TGAGTTATCA GCCACTCAGG	3925
Arg Ile Ser Ser Leu Glu Ser Glu Val	
1235 124	
CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT TAAGCGGCAG GCAGGATTGG	3985
CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC CCCAGTGACA GATGATGTCT	4045
TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA	4077

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1239 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly  
1 5 10 15

Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val  
20 25 30

Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val  
35 40 45

Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro  
50 55 60

Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln  
65 70 75 80

Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu  
85 90 95

Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser  
100 105 110

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val  
115 120 125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val  
130 135 140

Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr  
145 150 155 160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala  
165 170 175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser  
180 185 190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro  
195 200 205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe  
210 215 220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala  
 225 230 235 240  
 Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn  
 245 250 255  
 Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly  
 260 265 270  
 Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys  
 275 280 285  
 Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp  
 290 295 300  
 Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His  
 305 310 315 320  
 Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu  
 325 330 335  
 Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr  
 340 345 350  
 Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu  
 355 360 365  
 Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr  
 370 375 380  
 Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser  
 385 390 395 400  
 Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val  
 405 410 415  
 Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro  
 420 425 430  
 Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro  
 435 440 445  
 Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys  
 450 455 460  
 Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn  
 465 470 475 480  
 Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly  
 485 490 495  
 Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile  
 500 505 510  
 Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu  
 515 520 525  
 Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro  
 530 535 540  
 Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe  
 545 550 555 560  
 Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr  
 565 570 575

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Phe	Ser	Pro	Val	Ser	Tyr	Asn	Gln	Asn	Leu	Thr	Arg	Gly	Lys	Thr	Phe
580							585					590			
Thr	Ile	Gly	Lys	Ser	Val	Trp	Leu	Leu	Trp	Ala	Leu	Val	Phe	Asn	Asn
595							600					605			
Ser	Val	Pro	Ile	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser	Lys	Ile	Met	Val
610							615					620			
Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala	Arg	Tyr	Thr	Ala
625							630					635			640
Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Gln	Tyr	Ile	Asp	Thr	Val	Ser
645							645					650			655
Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln	Arg	Pro	Gln	Asp	Gln	Tyr	Pro	Pro
660							665					670			
Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg
675							680					685			
Ser	Asn	Tyr	Arg	Asp	Met	His	Thr	His	Met	Val	Lys	Phe	Asn	Gln	Arg
690							695					700			
Ser	Val	Glu	Asp	Ala	Leu	Thr	Ser	Leu	Lys	Met	Gly	Ser	Glu	Ala	Gln
705							710					715			720
Pro	Val	Pro	Arg	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu
725							725					730			735
Asn	Tyr	Met	Ala	Gly	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly
740							745					750			
Ser	Gly	Lys	Val	Phe	Ala	Thr	Thr	Gly	Tyr	Ile	Ala	Met	Gln	Lys	
755							760					765			
Asp	Ser	His	Trp	Lys	Arg	Ala	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu
770							775					780			
Gly	Asp	Gly	Glu	Thr	Gln	Lys	Leu	Glu	Thr	Val	Trp	Leu	Ser	Gly	Ile
785							790					795			800
Cys	Gln	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp
805							810					815			
Asn	Met	Gly	Gly	Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ala
820							825					830			
Leu	Leu	Val	Phe	Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Lys	Leu	Arg	His
835							840					845			
Ser	Val	Pro	Asn	Ser	Ser	Gln	Leu	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg
850							855					860			
Gly	Ile	Tyr	Ser	Cys	Phe	Ser	Gly	Val	Gln	Ser	Leu	Ala	Ser	Pro	Pro
865							870					875			880
Arg	Gln	Ala	Ser	Pro	Asp	Leu	Thr	Ala	Ser	Ser	Ala	Gln	Ala	Ser	Val
885							885					890			895
Leu	Lys	Ile	Leu	Gln	Ala	Ala	Arg	Asp	Met	Val	Thr	Thr	Ala	Gly	Val
900							905					910			
Ser	Asn	Ser	Leu	Asp	Arg	Ala	Thr	Arg	Thr	Ile	Glu	Asn	Trp	Gly	Gly
915							920					925			

Gly Arg Arg Ala Pro Pro Pro Ser Pro Cys Pro Thr Pro Arg Ser Gly  
930 935 940

Pro Ser Pro Cys Leu Pro Thr Pro Asp Pro Pro Pro Glu Pro Ser Pro  
945 950 955 960

Thr Gly Trp Gly Pro Pro Asp Gly Gly Arg Ala Ala Leu Val Arg Arg  
965 970 975

Ala Pro Gln Pro Pro Gly Arg Pro Pro Thr Pro Gly Pro Pro Leu Ser  
980 985 990

Asp Val Ser Arg Val Ser Arg Arg Pro Ala Trp Glu Ala Arg Trp Pro  
995 1000 1005

Val Arg Thr Gly His Cys Gly Arg His Leu Ser Ala Ser Glu Arg Pro  
1010 1015 1020

Leu Ser Pro Ala Arg Cys His Tyr Ser Ser Phe Pro Arg Ala Asp Arg  
1025 1030 1035 1040

Ser Gly Arg Pro Phe Leu Pro Leu Phe Pro Glu Pro Pro Glu Leu Glu  
1045 1050 1055

Asp Leu Pro Leu Leu Gly Pro Glu Gln Leu Ala Arg Arg Glu Ala Leu  
1060 1065 1070

Leu Asn Ala Ala Trp Ala Arg Gly Ser Arg Pro Ser His Ala Ser Leu  
1075 1080 1085

Pro Ser Ser Val Ala Glu Ala Phe Ala Arg Pro Ser Ser Leu Pro Ala  
1090 1095 1100

Gly Cys Thr Gly Pro Ala Cys Ala Arg Pro Asp Gly His Ser Ala Cys  
1105 1110 1115 1120

Arg Arg Leu Ala Gln Ala Gln Ser Met Cys Leu Pro Ile Tyr Arg Glu  
1125 1130 1135

Ala Cys Gln Glu Gly Glu Gln Ala Gly Ala Pro Ala Trp Gln His Arg  
1140 1145 1150

Gln His Val Cys Leu His Ala His Ala His Leu Pro Leu Cys Trp Gly  
1155 1160 1165

Ala Val Cys Pro His Leu Pro Pro Cys Asp Ser His Gly Ser Trp Leu  
1170 1175 1180

Ser Gly Ala Trp Gly Pro Leu Gly His Ser Gly Arg Thr Leu Gly Leu  
1185 1190 1195 1200

Gly Thr Gly Tyr Arg Asp Ser Gly Gly Leu Asp Glu Ile Ser Ser Val  
1205 1210 1215

Ala Arg Gly Thr Gln Gly Phe Pro Gly Pro Cys Thr Trp Arg Arg Ile  
1220 1225 1230

Ser Ser Leu Glu Ser Glu Val  
1235

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4002 base pairs  
(B) TYPE: nucleic acid

(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 189..3833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCCTTAATAA GATTTGCNAC GTACACTCGA GCCATCGCGA GTGTCCTTGA	60
ACGGTGGCTC TCGCTGCTCG CGCCCCCTCC TCCCGCGGGG GGAGCCTGAT	120
GCCACGTTCC	
CTATGAATTA TTTATGCCG GCCTAAAAAT ACCCCGAACT TCACAGCCCG	180
AGTGACCCTC	
CGGTGGAC ATG GGT GGG GCC CTG GGG CCG GCC CTG TTG CTC ACC TCG CTC	230
Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu	
1 5 10	
TTC GGT GCC TGG GCA GGG CTG GGT CCG GGG CAG GGC GAG CAG GGC ATG	278
Phe Gly Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met	
15 20 25 30	
ACG GTG GCC GTG GTG TTT AGC AGC TCA GGG CCG CCC CAG GCC CAG TTC	326
Thr Val Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe	
35 40 45	
CGT GTC CGC CTC ACC CCC CAG AGC TTC CTG GAC CTA CCC CTG GAG ATC	374
Arg Val Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile	
50 55 60	
CAG CCG CTC ACA GTT GGG GTC AAC ACC ACC AAC CCC AGC AGC CTC CTC	422
Gln Pro Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu	
65 70 75	
ACC CAG ATC TGC GGC CTC CTG GGT GCT GCC CAC GTC CAC GGC ATT GTC	470
Thr Gln Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val	
80 85 90	
TTT GAG GAC AAC GTG GAC ACC GAG GCG GTG GCC CAG ATC CTT GAC TTC	518
Phe Glu Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe	
95 100 105 110	
ATC TCC TCC CAG ACC CAT GTG CCC ATC CTC AGC ATC AGC GGA GGC TCT	566
Ile Ser Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser	
115 120 125	
GCT GTG GTC CTC ACC CCC AAG GAG CCG GGC TCC GCC TTC CTG CAG CTG	614
Ala Val Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu	
130 135 140	
GGC GTG TCC CTG GAG CAG CAG CTG CAG GTG CTG TTC AAG GTG CTG GAA	662
Gly Val Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu	
145 150 155	
GAG TAC GAC TGG AGC GCC TTC GCC GTC ATC ACC AGC CTG CAC CCG GGC	710
Glu Tyr Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly	
160 165 170	
CAC GCG CTC TTC CTG GAG GGC GTG CGC GCC GTC GCC GAC GCC AGC CAC	758
His Ala Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His	
175 180 185 190	

GTG AGT TGG CGG CTG CTG GAC GTG GTC ACG CTG GAA CTG GAC CCG GGA Val Ser Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly 195 200 205	806
GGG CCG CGC GCG CGC ACG CAG CGC CTG CTG CGC CAG CTC GAC GCG CCC Gly Pro Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro 210 215 220	854
GTG TTT GTG GCC TAC TGC TCG CGC GAG GAG GCC GAG GTG CTC TTC GCC Val Phe Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala 225 230 235	902
GAG GCG GCG CAG GCC GGT CTG GTG GGG CCC GGC CAC GTG TGG CTG GTG Glu Ala Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val 240 245 250	950
CCC AAC CTG GCG CTG GGC AGC ACC GAT GCG CCC CCC GCC ACC TTC CCC Pro Asn Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro 255 260 265 270	998
GTG GGC CTC ATC AGC GTC GTC ACC GAG AGC TGG CGC CTC AGC CTG CGC Val Gly Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg 275 280 285	1046
CAG AAG GTG CGC GAC GGC GTG GCC ATT CTG GCC CTG GGC GCC CAC AGC Gln Lys Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser 290 295 300	1094
TAC TGG CGC CAG CAT GGA ACC CTG CCA GCC CCG GCC GGG GAC TGC CGT Tyr Trp Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg 305 310 315	1142
GTT CAC CCT GGG CCC GTC AGC CCT GCC CGG GAG GCC TTC TAC AGG CAC Val His Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His 320 325 330	1190
CTA CTG AAT GTC ACC TGG GAG GGC CGA GAC TTC TCC TTC AGC CCT GGT Leu Leu Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly 335 340 345 350	1238
GGG TAC CTG GTC CAG CCC ACC ATG GTG GTG ATC GCC CTC AAC CGG CAC Gly Tyr Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His 355 360 365	1286
CGC CTC TGG GAG ATG GTG GGG CGC TGG GAG CAT GGC GTC CTA TAC ATG Arg Leu Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met 370 375 380	1334
AAG TAC CCC GTG TGG CCT CGC TAC AGT GCC TCT CTG CAG CCT GTG GTG Lys Tyr Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val 385 390 395	1382
GAC AGT CGG CAC CTG ACG GTG GCC ACG CTG GAA GAG CGG CCC TTT GTC Asp Ser Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val 400 405 410	1430
ATC GTG GAG AGC CCT GAC CCT GGC ACA GGA GGC TGT GTC CCC AAC ACC Ile Val Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr 415 420 425 430	1478
GTG CCC TGC CGC AGG CAG AGC AAC CAC ACC TTC AGC AGC GGG GAC GTG Val Pro Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val 435 440 445	1526
GCC CCC TAC ACC AAG CTC TGC TGT AAG GGA TTC TGC ATC GAC ATC CTC Ala Pro Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu 450 455 460	1574

AAG AAG CTG GCC AGA GTG GTC AAA TTC TCC TAC GAC CTG TAC CTG GTG Lys Lys Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val 465 470 475	1622
ACC AAC GGC AAG CAT GGC AAG CGG GTG CGC GGC GTA TGG AAC GGC ATG Thr Asn Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met 480 485 490	1670
ATT GGG GAG GTG TAC TAC AAG CGG GCA GAC ATG GCC ATC GGC TCC CTC Ile Gly Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu 495 500 505 510	1718
ACC ATC AAT GAG GAA CGC TCC GAG ATC GTA GAC TTC TCT GTA CCC TTT Thr Ile Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe 515 520 525	1766
GTG GAG ACG GGC ATC AGT GTG ATG GTG GCT CGC AGC AAT GGC ACC GTC Val Glu Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val 530 535 540	1814
TCC CCC TCG GCC TTC TTG GAG CCA TAT AGC CCT GCA GTG TGG GTG ATG Ser Pro Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met 545 550 555	1862
ATG TTT GTC ATG TGC CTC ACT GTG GTG GCC ATC ACC GTC TTC ATG TTC Met Phe Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe 560 565 570	1910
GAG TAC TTC AGC CCT GTC AGC TAC AAC CAG AAC CTC ACC AGA GGC AAG Glu Tyr Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys 575 580 585 590	1958
ACT TTC ACT ATC GGC AAG TCC GTG TGG CTG CTG TGG GCG CTG GTC TTC Thr Phe Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe 595 600 605	2006
AAC AAC TCA GTG CCC ATC GAG AAC CCG CGG GGC ACC ACC AGC AAG ATC Asn Asn Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile 610 615 620	2054
ATG GTT CTG GTC TGG GCC TTC TTT GCT GTC ATC TTC CTC GCC AGA TAC Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr 625 630 635	2102
ACG GCC AAC CTG GCC GCC TTC ATG ATC CAA GAG CAA TAC ATC GAC ACT Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr 640 645 650	2150
GTG TCG GGC CTC AGT GAC AAG AAG TTT CAG CGG CCT CAA GAT CAG TAC Val Ser Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr 655 660 665 670	2198
CCA CCT TTC CGC TTC GGC ACG GTG CCC AAC GGC AGC ACG GAG CGG AAC Pro Pro Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn 675 680 685	2246
ATC CGC AGT AAC TAC CGT GAC ATG CAC ACC CAC ATG GTC AAG TTC AAC Ile Arg Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn 690 695 700	2294
CAG CGC TCG GTG GAG GAC GCG CTC ACC AGC CTC AAG ATG GGC AAG GAC Gln Arg Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp 705 710 715	2342
GAG GGC TGC AAG CTG GTC ACC ATT GGG TCT GGC AAG GTC TTT GCT ACC Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr 720 725 730	2390

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ACT GGC TAC GGC ATC GCC ATG CAG AAG GAC TCC CAC TGG AAG CGG GCC	2438
Thr Gly Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala	
735 740 745 750	
ATA GAC CTG GCG CTC TTG CAG TTC CTG GGG GAC GGA GAG ACA CAG AAA	2486
Ile Asp Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys	
755 760 765	
CTG GAG ACA GTG TGG CTC TCA GGG ATC TGC CAG AAT GAG AAG AAC GAG	2534
Leu Glu Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu	
770 775 780	
GTG ATG AGC AGC AAG CTG GAC ATC GAC AAC ATG GGA GGC GTC TTC TAC	2582
Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr	
785 790 795	
ATG CTG CTG GTG GCC ATG GGG CTG GCC CTG CTG GTC TTC GCC TGG GAG	2630
Met Leu Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu	
800 805 810	
CAC CTG GTC TAC TGG AAG CTG CGC CAC TCG GTG CCC AAC TCA TCC CAG	2678
His Leu Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln	
815 820 825 830	
CTG GAC TTC CTG CTG GCT TTC AGC AGG GGC ATC TAC AGC TGC TTC AGC	2726
Leu Asp Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser	
835 840 845	
GGG GTG CAG AGC CTC GCC AGC CCA CCG CGG CAG GCC AGC CCG GAC CTC	2774
Gly Val Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu	
850 855 860	
ACG GCC AGC TCG GCC CAG GCC AGC GTG CTC AAG ATT CTG CAG GCA GCC	2822
Thr Ala Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala	
865 870 875	
CGC GAC ATG GTG ACC ACG GCG GGC GTA AGC AAC TCC CTG GAC CGC GCC	2870
Arg Asp Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala	
880 885 890	
ACT CGC ACC ATC GAG AAT TGG GGT GGC GGC CGC CGT GCG CCC CCA CCG	2918
Thr Arg Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro	
895 900 905 910	
TCC CCC TGC CCG ACC CCG CGG TCT GGC CCC AGC CCA TGC CTG CCC ACC	2966
Ser Pro Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr	
915 920 925	
CCC GAC CCG CCC CCA GAG CCG AGC CCC ACG GGC TGG GGA CCG CCA GAC	3014
Pro Asp Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp	
930 935 940	
GGG GGT CGC GCG GCG CTT GTG CGC AGG GCT CCG CAG CCC CCG GGC CGC	3062
Gly Gly Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg	
945 950 955	
CCC CCG ACG CCG GGG CCG CCC CTG TCC GAC GTC TCC CGA GTG TCG CGC	3110
Pro Pro Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg	
960 965 970	
CGC CCA GCC TGG GAG GCG CGG TGG CCG GTG CGG ACC GGG CAC TGC GGG	3158
Arg Pro Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly	
975 980 985 990	
AGG CAC CTC TCG GCC TCC GAG CGG CCC CTG TCG CCC GCG CGC TGT CAC	3206
Arg His Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His	
995 1000 1005	

3254

Tyr Ser Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro  
 1010 1015 1020

3302

CTC TTC CCG GAG CCC CCG GAG CTG GAG GAC CTG CCG CTG CTC GGT CCG  
 Leu Phe Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro  
 1025 1030 1035

3350

GAG CAG CTG GCC CGG CGG GAG GCC CTG CTG AAC GCG GCC TGG GCC CGG  
 Glu Gln Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg  
 1040 1045 1050

3398

GGC TCG CGC CCG AGT CAC GCT TCC CTG CCC AGC TCC GTG GCC GAG GCC  
 Gly Ser Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala  
 1055 1060 1065 1070

3446

TTC GCT CGG CCC AGC TCG CTG CCC GCT GGG TGC ACC GGC CCC GCC TGC  
 Phe Ala Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys  
 1075 1080 1085

3494

GCC CGC CCC GAC GGC CAC TCG GCC TGC AGG CGC TTG GCG CAG GCG CAG  
 Ala Arg Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln  
 1090 1095 1100

3542

TCG ATG TGC TTG CCG ATC TAC CCG GAG GCC TGC CAG GAG GGC GAG CAG  
 Ser Met Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln  
 1105 1110 1115

3590

GCA GGG GCC CCC GCC TGG CAG CAC AGA CAG CAC GTC TGC CTG CAC GCC  
 Ala Gly Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala  
 1120 1125 1130

3638

CAC GCC CAC CTG CCA TTG TGC TGG GGG GCT GTC TGT CCT CAC CTT CCA  
 His Ala His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro  
 1135 1140 1145 1150

3686

CCC TGT GAC AGC CAC GGC TCC TGG CTC TCC GGC GCC TGG GGG CCT CTG  
 Pro Cys Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu  
 1155 1160 1165

3734

GGG CAC AGC GGC AGG ACT CTG GGG CTG GGC ACA GGC TAC AGA GAC AGT  
 Gly His Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser  
 1170 1175 1180

3782

GGG GGA CTG GAC GAG ATC AGC AGT GTA GCC CGT GGG ACG CAA GGC TTC  
 Gly Gly Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe  
 1185 1190 1195

3830

CCG GGA CCC TGC ACC TGG AGA CGG ATC TCC AGT CTG GAG TCA GAA GTG  
 Pro Gly Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val  
 1200 1205 1210

3890

TGAGTTATCA GCCACTCAGG CTCCGAGCCA GCTGGATTCT CTGCCTGCCA CTGTCAGGGT

3950

TAAGCGGCAG GCAGGATTGG CCCTTCTCTG GCTTCTACCA TGAAATCCTG GCCATGGCAC

4002

CCCCAGTGACA GATGATGTCT TCCATGGTCA TCAGTGACCT CAGCTAGCCT CA

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1214 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ\_ID NO:54:

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Met Gly Gly Ala Leu Gly Pro Ala Leu Leu Leu Thr Ser Leu Phe Gly
 1           5          10          15

Ala Trp Ala Gly Leu Gly Pro Gly Gln Gly Glu Gln Gly Met Thr Val
 20          25          30

Ala Val Val Phe Ser Ser Ser Gly Pro Pro Gln Ala Gln Phe Arg Val
 35          40          45

Arg Leu Thr Pro Gln Ser Phe Leu Asp Leu Pro Leu Glu Ile Gln Pro
 50          55          60

Leu Thr Val Gly Val Asn Thr Thr Asn Pro Ser Ser Leu Leu Thr Gln
 65          70          75          80

Ile Cys Gly Leu Leu Gly Ala Ala His Val His Gly Ile Val Phe Glu
 85          90          95

Asp Asn Val Asp Thr Glu Ala Val Ala Gln Ile Leu Asp Phe Ile Ser
100         105         110

Ser Gln Thr His Val Pro Ile Leu Ser Ile Ser Gly Gly Ser Ala Val
115         120         125

Val Leu Thr Pro Lys Glu Pro Gly Ser Ala Phe Leu Gln Leu Gly Val
130         135         140

Ser Leu Glu Gln Gln Leu Gln Val Leu Phe Lys Val Leu Glu Glu Tyr
145         150         155         160

Asp Trp Ser Ala Phe Ala Val Ile Thr Ser Leu His Pro Gly His Ala
165         170         175

Leu Phe Leu Glu Gly Val Arg Ala Val Ala Asp Ala Ser His Val Ser
180         185         190

Trp Arg Leu Leu Asp Val Val Thr Leu Glu Leu Asp Pro Gly Gly Pro
195         200         205

Arg Ala Arg Thr Gln Arg Leu Leu Arg Gln Leu Asp Ala Pro Val Phe
210         215         220

Val Ala Tyr Cys Ser Arg Glu Glu Ala Glu Val Leu Phe Ala Glu Ala
225         230         235         240

Ala Gln Ala Gly Leu Val Gly Pro Gly His Val Trp Leu Val Pro Asn
245         250         255

Leu Ala Leu Gly Ser Thr Asp Ala Pro Pro Ala Thr Phe Pro Val Gly
260         265         270

Leu Ile Ser Val Val Thr Glu Ser Trp Arg Leu Ser Leu Arg Gln Lys
275         280         285

Val Arg Asp Gly Val Ala Ile Leu Ala Leu Gly Ala His Ser Tyr Trp
290         295         300

Arg Gln His Gly Thr Leu Pro Ala Pro Ala Gly Asp Cys Arg Val His
305         310         315         320

Pro Gly Pro Val Ser Pro Ala Arg Glu Ala Phe Tyr Arg His Leu Leu
325         330         335

Asn Val Thr Trp Glu Gly Arg Asp Phe Ser Phe Ser Pro Gly Gly Tyr
340         345         350

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Leu Val Gln Pro Thr Met Val Val Ile Ala Leu Asn Arg His Arg Leu  
355 360 365

Trp Glu Met Val Gly Arg Trp Glu His Gly Val Leu Tyr Met Lys Tyr  
370 375 380

Pro Val Trp Pro Arg Tyr Ser Ala Ser Leu Gln Pro Val Val Asp Ser  
385 390 395 400

Arg His Leu Thr Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val  
405 410 415

Glu Ser Pro Asp Pro Gly Thr Gly Gly Cys Val Pro Asn Thr Val Pro  
420 425 430

Cys Arg Arg Gln Ser Asn His Thr Phe Ser Ser Gly Asp Val Ala Pro  
435 440 445

Tyr Thr Lys Leu Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys  
450 455 460

Leu Ala Arg Val Val Lys Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn  
465 470 475 480

Gly Lys His Gly Lys Arg Val Arg Gly Val Trp Asn Gly Met Ile Gly  
485 490 495

Glu Val Tyr Tyr Lys Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile  
500 505 510

Asn Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu  
515 520 525

Thr Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro  
530 535 540

Ser Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe  
545 550 555 560

Val Met Cys Leu Thr Val Val Ala Ile Thr Val Phe Met Phe Glu Tyr  
565 570 575

Phe Ser Pro Val Ser Tyr Asn Gln Asn Leu Thr Arg Gly Lys Thr Phe  
580 585 590

Thr Ile Gly Lys Ser Val Trp Leu Leu Trp Ala Leu Val Phe Asn Asn  
595 600 605

Ser Val Pro Ile Glu Asn Pro Arg Gly Thr Thr Ser Lys Ile Met Val  
610 615 620

Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Arg Tyr Thr Ala  
625 630 635 640

Asn Leu Ala Ala Phe Met Ile Gln Glu Gln Tyr Ile Asp Thr Val Ser  
645 650 655

Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Gln Asp Gln Tyr Pro Pro  
660 665 670

Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg  
675 680 685

Ser Asn Tyr Arg Asp Met His Thr His Met Val Lys Phe Asn Gln Arg  
690 695 700

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Ser Val Glu Asp Ala Leu Thr Ser Leu Lys Met Gly Lys Asp Glu Gly  
 705 710 715 720  
 Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Thr Thr Gly  
 725 730 735  
 Tyr Gly Ile Ala Met Gln Lys Asp Ser His Trp Lys Arg Ala Ile Asp  
 740 745 750  
 Leu Ala Leu Leu Gln Phe Leu Gly Asp Gly Glu Thr Gln Lys Leu Glu  
 755 760 765  
 Thr Val Trp Leu Ser Gly Ile Cys Gln Asn Glu Lys Asn Glu Val Met  
 770 775 780  
 Ser Ser Lys Leu Asp Ile Asp Asn Met Gly Gly Val Phe Tyr Met Leu  
 785 790 795 800  
 Leu Val Ala Met Gly Leu Ala Leu Leu Val Phe Ala Trp Glu His Leu  
 805 810 815  
 Val Tyr Trp Lys Leu Arg His Ser Val Pro Asn Ser Ser Gln Leu Asp  
 820 825 830  
 Phe Leu Leu Ala Phe Ser Arg Gly Ile Tyr Ser Cys Phe Ser Gly Val  
 835 840 845  
 Gln Ser Leu Ala Ser Pro Pro Arg Gln Ala Ser Pro Asp Leu Thr Ala  
 850 855 860  
 Ser Ser Ala Gln Ala Ser Val Leu Lys Ile Leu Gln Ala Ala Arg Asp  
 865 870 875 880  
 Met Val Thr Thr Ala Gly Val Ser Asn Ser Leu Asp Arg Ala Thr Arg  
 885 890 895  
 Thr Ile Glu Asn Trp Gly Gly Arg Arg Ala Pro Pro Pro Ser Pro  
 900 905 910  
 Cys Pro Thr Pro Arg Ser Gly Pro Ser Pro Cys Leu Pro Thr Pro Asp  
 915 920 925  
 Pro Pro Pro Glu Pro Ser Pro Thr Gly Trp Gly Pro Pro Asp Gly Gly  
 930 935 940  
 Arg Ala Ala Leu Val Arg Arg Ala Pro Gln Pro Pro Gly Arg Pro Pro  
 945 950 955 960  
 Thr Pro Gly Pro Pro Leu Ser Asp Val Ser Arg Val Ser Arg Arg Pro  
 965 970 975  
 Ala Trp Glu Ala Arg Trp Pro Val Arg Thr Gly His Cys Gly Arg His  
 980 985 990  
 Leu Ser Ala Ser Glu Arg Pro Leu Ser Pro Ala Arg Cys His Tyr Ser  
 995 1000 1005  
 Ser Phe Pro Arg Ala Asp Arg Ser Gly Arg Pro Phe Leu Pro Leu Phe  
 1010 1015 1020  
 Pro Glu Pro Pro Glu Leu Glu Asp Leu Pro Leu Leu Gly Pro Glu Gln  
 1025 1030 1035 1040  
 Leu Ala Arg Arg Glu Ala Leu Leu Asn Ala Ala Trp Ala Arg Gly Ser  
 1045 1050 1055

Arg Pro Ser His Ala Ser Leu Pro Ser Ser Val Ala Glu Ala Phe Ala  
 1060 1065 1070  
 Arg Pro Ser Ser Leu Pro Ala Gly Cys Thr Gly Pro Ala Cys Ala Arg  
 1075 1080 1085  
 Pro Asp Gly His Ser Ala Cys Arg Arg Leu Ala Gln Ala Gln Ser Met  
 1090 1095 1100  
 Cys Leu Pro Ile Tyr Arg Glu Ala Cys Gln Glu Gly Glu Gln Ala Gly  
 1105 1110 1115 1120  
 Ala Pro Ala Trp Gln His Arg Gln His Val Cys Leu His Ala His Ala  
 1125 1130 1135  
 His Leu Pro Leu Cys Trp Gly Ala Val Cys Pro His Leu Pro Pro Cys  
 1140 1145 1150  
 Asp Ser His Gly Ser Trp Leu Ser Gly Ala Trp Gly Pro Leu Gly His  
 1155 1160 1165  
 Ser Gly Arg Thr Leu Gly Leu Gly Thr Gly Tyr Arg Asp Ser Gly Gly  
 1170 1175 1180  
 Leu Asp Glu Ile Ser Ser Val Ala Arg Gly Thr Gln Gly Phe Pro Gly  
 1185 1190 1195 1200  
 Pro Cys Thr Trp Arg Arg Ile Ser Ser Leu Glu Ser Glu Val  
 1205 1210

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 5538 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: both
    - (D) TOPOLOGY: both
  - ii) MOLECULE TYPE: cDNA
  - ix) FEATURE:
    - (A) NAME/KEY: CDS
    - (B) LOCATION: 210 1664

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

TTGAAATTGCA ATCTCTTCAA GACACAAGAT TAAAACAAAAA TTTACGCTAA ATTGGATTTC	60
AAATTATCTT CCGTTCATTT ATCCTTCGTC TTTCTTATGT GGATATGCAA GCGAGAACAA	120
GGGACTGGAC ATTCCCAACA TGCTCACTCC CTTAATCTGT CCGTCTAGAG GTTTGGCTTC	180
TACAAACCAA GGGAGTCGAC GAGTTGAAG ATG AAG CCC AGA GCG GAG TGC TGT	233
Met Lys Pro Arg Ala Glu Cys Cys	
1 5	
TCT CCC AAG TTC TGG TTG GTG TTG GCC GTC CTG GCC GTG TCA GGC AGC	281
Ser Pro Lys Phe Trp Leu Val Leu Ala Val Leu Ala Val Ser Gly Ser	
10 15 20	
AGA GCT CGT TCT CAG AAG AGC CCC CCC AGC ATT GGC ATT GCT GTC ATC	329
Arg Ala Arg Ser Gln Lys Ser Pro Pro Ser Ile Gly Ile Ala Val Ile	
25 30 35 40	

CTC GTG GGC ACT TCC GAC GAG GTG GCC ATC AAG GAT GCC CAC GAG AAA Leu Val Gly Thr Ser Asp Glu Val Ala Ile Lys Asp Ala His Glu Lys 45 50 55	377
GAT GAT TTC CAC CAT CTC TCC GTG GTA CCC CGG GTG GAA CTG GTA GCC Asp Asp Phe His His Leu Ser Val Val Pro Arg Val Glu Leu Val Ala 60 65 70	425
ATG AAT GAG ACC GAC CCA AAG AGC ATC ATC ACC CGC ATC TGT GAT CTC Met Asn Glu Thr Asp Pro Lys Ser Ile Ile Thr Arg Ile Cys Asp Leu 75 80 85	473
ATG TCT GAC CGG AAG ATC CAG GGG GTG GTG TTT GCT GAT GAC ACA GAC Met Ser Asp Arg Lys Ile Gln Gly Val Val Phe Ala Asp Asp Thr Asp 90 95 100	521
CAG GAA GCC ATC GCC CAG ATC CTC GAT TTC ATT TCA GCA CAG ACT CTC Gln Glu Ala Ile Ala Gln Ile Leu Asp Phe Ile Ser Ala Gln Thr Leu 105 110 115 120	569
ACC CCG ATC CTG GGC ATC CAC GGG GGC TCC TCT ATG ATA ATG GCA GAT Thr Pro Ile Leu Gly Ile His Gly Ser Ser Met Ile Met Ala Asp 125 130 135	617
AAG GAT GAA TCC TCC ATG TTC CAG TTT GGC CCA TCA ATT GAA CAG Lys Asp Glu Ser Ser Met Phe Phe Gln Phe Gly Pro Ser Ile Glu Gln 140 145 150	665
CAA GCT TCC GTA ATG CTC AAC ATC ATG GAA GAA TAT GAC TGG TAC ATC Gln Ala Ser Val Met Leu Asn Ile Met Glu Glu Tyr Asp Trp Tyr Ile 155 160 165	713
TTT TCT ATC GTC ACC ACC TAT TTC CCT GGC TAC CAG GAC TTT GTA AAC Phe Ser Ile Val Thr Thr Tyr Phe Pro Gly Tyr Gln Asp Phe Val Asn 170 175 180	761
AAG ATC CGC AGC ACC ATT GAG AAT AGC TTT GTG GGC TGG GAG CTA GAG Lys Ile Arg Ser Thr Ile Glu Asn Ser Phe Val Gly Trp Glu Leu Glu 185 190 195 200	809
GAG GTC CTC CTA CTG GAC ATG TCC CTG GAC GAT GGA GAT TCT AAG ATC Glu Val Leu Leu Asp Met Ser Leu Asp Asp Gly Asp Ser Lys Ile 205 210 215	857
CAG AAT CAG CTC AAG AAA CTT CAA AGC CCC ATC ATT CTT CTT TAC TGT Gln Asn Gln Leu Lys Lys Leu Gln Ser Pro Ile Ile Leu Leu Tyr Cys 220 225 230	905
ACC AAG GAA GAA GCC ACC TAC ATC TTT GAA GTG GCC AAC TCA GTA GGG Thr Lys Glu Glu Ala Thr Tyr Ile Phe Glu Val Ala Asn Ser Val Gly 235 240 245	953
CTG ACT GGC TAT GGC TAC ACG TGG ATC GTG CCC AGT CTG GTG GCA GGG Leu Thr Gly Tyr Gly Tyr Thr Trp Ile Val Pro Ser Leu Val Ala Gly 250 255 260	1001
GAT ACA GAC ACA GTG CCT GCG GAG TTC CCC ACT GGG CTC ATC TCT GTA Asp Thr Asp Thr Val Pro Ala Glu Phe Pro Thr Gly Leu Ile Ser Val 265 270 275 280	1049
TCA TAT GAT GAA TGG GAC TAT GGC CTC CCC CCC AGA GTG AGA GAT GGA Ser Tyr Asp Glu Trp Asp Tyr Gly Leu Pro Pro Arg Val Arg Asp Gly 285 290 295	1097
ATT GCC ATA ATC ACC ACT GCT GCT TCT GAC ATG CTG TCT GAG CAC AGC Ile Ala Ile Ile Thr Thr Ala Ala Ser Asp Met Leu Ser Glu His Ser 300 305 310	1145

TTC ATC CCT GAG CCC AAA AGC AGT TGT TAC AAC ACC CAC GAG AAG AGA Phe Ile Pro Glu Pro Lys Ser Ser Cys Tyr Asn Thr His Glu Lys Arg 315 320 325	1193
ATC TAC CAG TCC AAT ATG CTA AAT AGG TAT CTG ATC AAT GTC ACT TTT Ile Tyr Gln Ser Asn Met Leu Asn Arg Tyr Leu Ile Asn Val Thr Phe 330 335 340	1241
GAG GGG AGG AAT TTG TCC TTC AGT GAA GAT GGC TAC CAG ATG CAC CCG Glu Gly Arg Asn Leu Ser Phe Ser Glu Asp Gly Tyr Gln Met His Pro 345 350 355 360	1289
AAA CTG GTG ATA ATT CTT CTG AAC AAG GAG AGG AAG TGG GAA AGG GTG Lys Leu Val Ile Ile Leu Asn Lys Glu Arg Lys Trp Glu Arg Val 365 370 375	1337
GGG AAG TGG AAA GAC AAG TCC CTG CAG ATG AAG TAC TAT GTG TGG CCC Gly Lys Trp Lys Asp Lys Ser Leu Gln Met Lys Tyr Tyr Val Trp Pro 380 385 390	1385
CGA ATG TGT CCA GAG ACT GAA GAG CAG GAG GAT GAC CAT CTG AGC ATT Arg Met Cys Pro Glu Thr Glu Glu Gln Glu Asp Asp His Leu Ser Ile 395 400 405	1433
GTG ACC CTG GAG GAG GCA CCA TTT GTC ATT GTG GAA AGT GTG GAC CCT Val Thr Leu Glu Glu Ala Pro Phe Val Ile Val Glu Ser Val Asp Pro 410 415 420	1481
CTG AGT GGA ACC TGC ATG AGG AAC ACA GTC CCC TGC CAA AAA CGC ATA Leu Ser Gly Thr Cys Met Arg Asn Thr Val Pro Cys Gln Lys Arg Ile 425 430 435 440	1529
GTC ACT GAG AAT AAA ACA GAC GAG GAG CCG GGT TAC ATC AAA AAA TGC Val Thr Glu Asn Lys Thr Asp Glu Glu Pro Gly Tyr Ile Lys Lys Cys 445 450 455	1577
TGC AAG GGG TTC TGT ATT GAC ATC CTT AAG AAA ATT TCT AAA TCT GTG Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Lys Ile Ser Lys Ser Val 460 465 470	1625
AAG TTC ACC TAT GAC CTT TAC CTG GTT ACC AAT GGC AAG CAT GGG AAG Lys Phe Thr Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys His Gly Lys 475 480 485	1673
AAA ATC AAT GGA ACC TGG AAT GGT ATG ATT GGA GAG GTG GTC ATG AAG Lys Ile Asn Gly Thr Trp Asn Gly Met Ile Gly Glu Val Val Met Lys 490 495 500	1721
AGG GCC TAC ATG GCA GTG GGC TCA CTC ACC ATC AAT GAG GAA CGA TCG Arg Ala Tyr Met Ala Val Gly Ser Leu Thr Ile Asn Glu Glu Arg Ser 505 510 515 520	1769
GAG GTG GTC GAC TTC TCT GTG CCC TTC ATA GAG ACA GGC ATC AGT GTC Glu Val Val Asp Phe Ser Val Pro Phe Ile Glu Thr Gly Ile Ser Val 525 530 535	1817
ATG GTG TCA CGC AGC AAT GGG ACT GTC TCA CCT TCT GCC TTC TTA GAG Met Val Ser Arg Ser Asn Gly Thr Val Ser Pro Ser Ala Phe Leu Glu 540 545 550	1865
CCA TTC AGC GCT GAC GTA TGG GTG ATG ATG TTT GTG ATG CTG CTC ATC Pro Phe Ser Ala Asp Val Trp Val Met Met Phe Val Met Leu Leu Ile 555 560 565	1913
GTC TCA GCC GTG GCT GTC TTT GTC TTT GAG TAC TTC AGC CCT GTG GGT Val Ser Ala Val Ala Val Phe Val Phe Glu Tyr Phe Ser Pro Val Gly 570 575 580	1961

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TAT AAC AGG TGC CTC GCT GAT GGC AGA GAG CCT GGT GGA CCC TCT TTC Tyr Asn Arg Cys Leu Ala Asp Gly Arg Glu Pro Gly Gly Pro Ser Phe 585 590 595 600	2009
ACC ATC GGC AAA GCT ATT TGG TTG CTC TGG GGT CTG GTG TTT AAC AAC Thr Ile Gly Lys Ala Ile Trp Leu Leu Trp Gly Leu Val Phe Asn Asn 605 610 615	2057
TCC GTA CCT GTG CAG AAC CCA AAG GGG ACC ACC TCC AAG ATC ATG GTG Ser Val Pro Val Gln Asn Pro Lys Gly Thr Thr Ser Lys Ile Met Val 620 625 630	2105
TCA GTG TGG GCC TTC TTT GCT GTC ATC TTC CTG GCC AGC TAC ACT GCC Ser Val Trp Ala Phe Ala Val Ile Phe Leu Ala Ser Tyr Thr Ala 635 640 645	2153
AAC TTA GCT GCC TTC ATG ATC CAA GAG GAA TAT GTG GAC CAG GTT TCT Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp Gln Val Ser 650 655 660	2201
GGC CTG AGC GAC AAA AAG TTC CAG AGA CCT AAT GAC TTC TCA CCC CCT Gly Leu Ser Asp Lys Lys Phe Gln Arg Pro Asn Asp Phe Ser Pro Pro 665 670 675 680	2249
TTC CGC TTT GGG ACC GTG CCC AAC GGC AGC ACA GAG AGA AAT ATT CGC Phe Arg Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Arg Asn Ile Arg 685 690 695	2297
AAT AAC TAT GCA GAA ATG CAT GCC TAC ATG GGA AAG TTC AAC CAG AGG Asn Asn Tyr Ala Glu Met His Ala Tyr Met Gly Lys Phe Asn Gln Arg 700 705 710	2345
GGT GTA GAT GAT GCA TTG CTC TCC CTG AAA ACA GGG AAA CTG GAT GCC Gly Val Asp Asp Ala Leu Leu Ser Leu Lys Thr Gly Lys Leu Asp Ala 715 720 725	2393
TTC ATC TAT GAT GCA GCA GTG CTG AAC TAT ATG GCA GGC AGA GAT GAA Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Gly Arg Asp Glu 730 735 740	2441
GGC TGC AAG CTG GTG ACC ATT GGC AGT GGG AAG GTC TTT GCT TCC ACT Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe Ala Ser Thr 745 750 755 760	2489
GGC TAT GGC ATT GCC ATC CAA AAA GAT TCT GGG TGG AAG CGC CAG GTG Gly Tyr Gly Ile Ala Ile Gln Lys Asp Ser Gly Trp Lys Arg Gln Val 765 770 775	2537
GAC CTT GCT ATC CTG CAG CTC TTT GGA GAT GGG GAG ATG GAA GAA CTG Asp Leu Ala Ile Leu Gln Leu Phe Gly Asp Gly Glu Met Glu Glu Leu 780 785 790	2585
GAA GCT CTC TGG CTC ACT GGC ATT TGT CAC AAT GAG AAG AAT GAG GTC Glu Ala Leu Trp Leu Thr Gly Ile Cys His Asn Glu Lys Asn Glu Val 795 800 805	2633
ATG AGC AGC CAG CTG GAC ATT GAC AAC ATG GCA GGG GTC TTC TAC ATG Met Ser Ser Gln Leu Asp Ile Asp Asn Met Ala Gly Val Phe Tyr Met 810 815 820	2681
TTG GGG GCG GCC ATG GCT CTC AGC CTC ATC ACC TTC ATC TGC GAA CAC Leu Gly Ala Ala Met Ala Leu Ser Leu Ile Thr Phe Ile Cys Glu His 825 830 835 840	2729
CTT TTC TAT TGG CAG TTC CGA CAT TGC TTT ATG GGT GTC TGT TCT GGC Leu Phe Tyr Trp Gln Phe Arg His Cys Phe Met Gly Val Cys Ser Gly 845 850 855	2777

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AAG CCT GGC ATG GTC TTC TCC ATC AGC AGA GGT ATC TAC AGC TGC ATC Lys Pro Gly Met Val Phe Ser Ile Ser Arg Gly Ile Tyr Ser Cys Ile 860 865 870	2825
CAT GGG GTG GCG ATC GAG GAG CGC CAG TCT GTA ATG AAC TCC CCC ACC His Gly Val Ala Ile Glu Glu Arg Gln Ser Val Met Asn Ser Pro Thr 875 880 885	2873
GCA ACC ATG AAC AAC ACA CAC TCC AAC ATC CTG CGC CTG CTG CGC ACG Ala Thr Met Asn Asn Thr His Ser Asn Ile Leu Arg Leu Leu Arg Thr 890 895 900	2921
GCC AAG AAC ATG GCT AAC CTG TCT GGT GTG AAT GGC TCA CCG CAG AGC Ala Lys Asn Met Ala Asn Leu Ser Gly Val Asn Gly Ser Pro Gln Ser 905 910 915 920	2969
GCC CTG GAC TTC ATC CGA CGG GAG TCA TCC GTC TAT GAC ATC TCA GAG Ala Leu Asp Phe Ile Arg Arg Glu Ser Ser Val Tyr Asp Ile Ser Glu 925 930 935	3017
CAC CGC CGC AGC TTC ACG CAT TCT GAC TGC AAA TCC TAC AAC AAC CCG His Arg Arg Ser Phe Thr His Ser Asp Cys Lys Ser Tyr Asn Asn Pro 940 945 950	3065
CCC TGT GAG GAG AAC CTC TTC AGT GAC TAC ATC AGT GAG GTA GAG AGA Pro Cys Glu Glu Asn Leu Phe Ser Asp Tyr Ile Ser Glu Val Glu Arg 955 960 965	3113
ACG TTC GGG AAC CTG CAG CTG AAG GAC AGC AAC GTG TAC CAA GAT CAC Thr Phe Gly Asn Leu Gln Leu Lys Asp Ser Asn Val Tyr Gln Asp His 970 975 980	3161
TAC CAC CAT CAC CAC CGG CCC CAT AGT ATT GGC AGT GCC AGC TCC ATC Tyr His His His Arg Pro His Ser Ile Gly Ser Ala Ser Ser Ile 985 990 995 1000	3209
GAT GGG CTC TAC GAC TGT GAC AAC CCA CCC TTC ACC ACC CAG TCC AGG Asp Gly Leu Tyr Asp Cys Asp Asn Pro Pro Phe Thr Thr Gln Ser Arg 1005 1010 1015	3257
TCC ATC AGC AAG AAG CCC CTG GAC ATC GGC CTC CCC TCC TCC AAG CAC Ser Ile Ser Lys Lys Pro Leu Asp Ile Gly Leu Pro Ser Ser Lys His 1020 1025 1030	3305
AGC CAG CTC AGT GAC CTG TAC GGC AAA TTC TCC TTC AAG AGC GAC CGC Ser Gln Leu Ser Asp Leu Tyr Gly Lys Phe Ser Phe Lys Ser Asp Arg 1035 1040 1045	3353
TAC AGT GGC CAC GAC GAC TTG ATC CGC TCC GAT GTC TCT GAC ATC TCA Tyr Ser Gly His Asp Asp Leu Ile Arg Ser Asp Val Ser Asp Ile Ser 1050 1055 1060	3401
ACC CAC ACC GTC ACC TAT GGG AAC ATC GAG GGC AAT GCC GCC AAG AGG Thr His Thr Val Thr Tyr Gly Asn Ile Glu Gly Asn Ala Ala Lys Arg 1065 1070 1075 1080	3449
CGT AAG CAG CAA TAT AAG GAC AGC CTG AAG AAG CGG CCT GCC TCG GCC Arg Lys Gln Gln Tyr Lys Asp Ser Leu Lys Lys Arg Pro Ala Ser Ala 1085 1090 1095	3497
AAG TCC CGC AGG GAG TTT GAC GAG ATC GAG CTG GCC TAC CGT CGC CGA Lys Ser Arg Arg Glu Phe Asp Glu Ile Glu Leu Ala Tyr Arg Arg Arg 1100 1105 1110	3545
CCG CCC CGC TCC CCT GAC CAC AAG CGC TAC TTC AGG GAC AAG GAA GGG Pro Pro Arg Ser Pro Asp His Lys Arg Tyr Phe Arg Asp Lys Glu Gly 1115 1120 1125	3593

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CTA CGG GAC TTC TAC CTG GAC CAG TTC CGA ACA AAG GAG AAC TCA CCC Leu Arg Asp Phe Tyr Leu Asp Gln Phe Arg Thr Lys Glu Asn Ser Pro 1130 1135 1140	3641
CAC TGG GAG CAC GTA GAC CTG ACC GAC ATC TAC AAG GAG CGG AGT GAT His Trp Glu His Val Asp Leu Thr Asp Ile Tyr Lys Glu Arg Ser Asp 1145 1150 1155 1160	3689
GAC TTT AAG CGC GAC TCC ATC AGC GGA GGA GGG CCC TGT ACC AAC AGG Asp Phe Lys Arg Asp Ser Ile Ser Gly Gly Pro Cys Thr Asn Arg 1165 1170 1175	3737
TCT CAC ATC AAG CAC GGG ACG GGC GAC AAA CAC GGC GTG GTC AGC GGG Ser His Ile Lys His Gly Thr Gly Asp Lys His Gly Val Val Ser Gly 1180 1185 1190	3785
GTA CCT GCA CCT TGG GAG AAG AAC CTG ACC AAC GTG GAG TGG GAG GAC Val Pro Ala Pro Trp Glu Lys Asn Leu Thr Asn Val Glu Trp Glu Asp 1195 1200 1205	3833
CGG TCC GGG GGC AAC TTC TGC CGC AGC TGT CCC TCC AAG CTG CAC AAC Arg Ser Gly Gly Asn Phe Cys Arg Ser Cys Pro Ser Lys Leu His Asn 1210 1215 1220	3881
TAC TCC ACG ACG GTG ACG GGT CAG AAC TCG GGC AGG CAG GCG TGC ATC Tyr Ser Thr Thr Val Thr Gly Gln Asn Ser Gly Arg Gln Ala Cys Ile 1225 1230 1235 1240	3929
CGG TGT GAG GCT TGC AAG AAA GCA GGC AAC CTG TAT GAC ATC AGT GAG Arg Cys Glu Ala Cys Lys Ala Gly Asn Leu Tyr Asp Ile Ser Glu 1245 1250 1255	3977
GAC AAC TCC CTG CAG GAA CTG GAC CAG CCG GCT GCC CCA GTG GCG GTG Asp Asn Ser Leu Gin Glu Leu Asp Gin Pro Ala Ala Pro Val Ala Val 1260 1265 1270	4025
ACG TCA AAC GCC TCC ACC ACT AAG TAC CCT CAG AGC CCG ACT AAT TCC Thr Ser Asn Ala Ser Thr Thr Lys Tyr Pro Gln Ser Pro Thr Asn Ser 1275 1280 1285	4073
AAG GCC CAG AAG AAG AAC CGG AAC AAA CTG CGC CGG CAG CAC TCC TAC Lys Ala Gln Lys Lys Asn Arg Asn Lys Leu Arg Arg Gln His Ser Tyr 1290 1295 1300	4121
GAC ACC TTC GTG GAC CTG CAG AAG GAA GAA GCC GCC CTG GCC CCG CGC Asp Thr Phe Val Asp Leu Gln Lys Glu Ala Ala Leu Ala Pro Arg 1305 1310 1315 1320	4169
AGC GTA AGC CTG AAA GAC AAG GGC CGA TTC ATG GAT GGG AGC CCC TAC Ser Val Ser Leu Lys Asp Lys Gly Arg Phe Met Asp Gly Ser Pro Tyr 1325 1330 1335	4217
GCC CAC ATG TTT GAG ATG TCA GCT GGC GAG AGC ACC TTT GCC AAC AAC Ala His Met Phe Glu Met Ser Ala Gly Glu Ser Thr Phe Ala Asn Asn 1340 1345 1350	4265
AAG TCC TCA GTG CCC ACT GCC GGA CAT CAC CAC AAC AAC CCC GGC Lys Ser Ser Val Pro Thr Ala Gly His His His Asn Asn Pro Gly 1355 1360 1365	4313
GGC GGG TAC ATG CTC AGC AAG TCG CTC TAC CCT GAC CGG GTC ACG CAA Gly Gly Tyr Met Leu Ser Lys Ser Leu Tyr Pro Asp Arg Val Thr Gln 1370 1375 1380	4361
AAC CCT TTC ATC CCC ACT TTT GGG GAC GAC CAG TGC TTG CTC CAT GGC Asn Pro Phe Ile Pro Thr Phe Gly Asp Asp Gln Cys Leu Leu His Gly 1385 1390 1395 1400	4409

AGC AAA TCC TAC TTC AGG CAG CCC ACG GTG GCG GGG GCG TCG AAA Ser Lys Ser Tyr Phe Phe Arg Gln Pro Thr Val Ala Gly Ala Ser Lys 1405 1410 1415	4457
GCC AGG CCG GAC TTC CGG GCC CTT GTC ACC AAC AAG CCG GTG GTC TCG Ala Arg Pro Asp Phe Arg Ala Leu Val Thr Asn Lys Pro Val Val Ser 1420 1425 1430	4505
GCC CTT CAT GGG GCC GTG CCA GCC CGT TTC CAG AAG GAC ATC TGT ATA Ala Leu His Gly Ala Val Pro Ala Arg Phe Gln Lys Asp Ile Cys Ile 1435 1440 1445	4553
GGG AAC CAG TCC AAC CCC TGT GTG CCT AAC AAC ACA AAC CCC AGG GCT Gly Asn Gln Ser Asn Pro Cys Val Pro Asn Asn Thr Asn Pro Arg Ala 1450 1455 1460	4601
TTC AAT GGC TCC AGC AAT GGG CAT GTT TAT GAG AAA CTT TCT AGT ATT Phe Asn Gly Ser Ser Asn Gly His Val Tyr Glu Lys Leu Ser Ser Ile 1465 1470 1475 1480	4649
GAG TCT GAT GTC TGAGTGAGGG AACAGAGAGG TTAAGGTGGG TACGGGAGGG Glu Ser Asp Val 148	4701
TAAGGCTGTG GGTCGCGTGA TGCGCATGTC ACGGAGGGTG ACGGGGGTGA ACTTGGTTCC CATTGCTCC TTTCTTGTAA TAATTATTT ATGGGATCCT GGAGTTCTGG TTCCTACTGG GGGCAACCCT GGTGACCAGC ACCATCTCTC CTCCTTTCA CAGTTCTCTC CTTCTCCCC CCGCTGTCAG CCATTCTGT TCCCAGAGA TGATGCCATG GGCCCTCTCA GCAGGGGAGG GTAGAGCGGA GAAAGGAAGG GCTGCATGCG GGCTTCTCC TGGTGTGGAA GAGCTCCTTG ATATCCTCTT TGAGTGAAGC TGGGAGAACC AAAAAGAGGC TATGTGAGCA CAAAGGTAGC TTTTCCAAA CTGATCTTT CATTAGGTG AGGAAGCAA AGCATCTATG TGAGACCATT TAGCACACTG CTTGTGAAAG GAAAGAGGCT CTGGCTAAAT TCATGCTGCT TAGATGACAT CTGTCTAGGA ATCATGTGCC AAGCAGAGGT TGGGAGGCCA TTTGTGTTA TATATAAGCC AAAAATGCT TGCTTCAACC CCATGAGACT CGATAGTGGT GGTGAACAGA ACCCAAGGTC ATTGGTGGCA GAGTGGATTTC TTGAACAAAC TGGAAAGTAC GTTATGATAG TGTCCCCCGG TGCCTTGGGG ACAAGAGCAG GTGGATTGTG CGTGCATGTG TGTTCATGCA CACTTGCACC CATGTGTAGT CAGGTGCCTC AAGAGAAGGC AACCTTGACT CTTTCGTTGA ATTTGCATCT CTTCAAGACA CAAGATTAAA ACAAAATTAA CGCTAAATTG GATTTAAAT TATCTTC	4761 4821 4881 4941 5001 5061 5121 5181 5241 5301 5361 5421 5481 5538

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1484 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Pro Arg Ala Glu Cys Cys Ser Pro Lys Phe Trp Leu Val Leu  
1 5 10 15

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Ala	Val	Leu	Ala	Val	Ser	Gly	Ser	Arg	Ala	Arg	Ser	Gln	Lys	Ser	Pro
20							25					30			
Pro	Ser	Ile	Gly	Ile	Ala	Val	Ile	Leu	Val	Gly	Thr	Ser	Asp	Glu	Val
35							40				45				
Ala	Ile	Lys	Asp	Ala	His	Glu	Lys	Asp	Asp	Phe	His	His	Leu	Ser	Val
50						55				60					
Val	Pro	Arg	Val	Glu	Leu	Val	Ala	Met	Asn	Glu	Thr	Asp	Pro	Lys	Ser
65						70				75			80		
Ile	Ile	Thr	Arg	Ile	Cys	Asp	Leu	Met	Ser	Asp	Arg	Lys	Ile	Gln	Gly
85							90				95				
Val	Val	Phe	Ala	Asp	Asp	Thr	Asp	Gln	Glu	Ala	Ile	Ala	Gln	Ile	Leu
100							105				110				
Asp	Phe	Ile	Ser	Ala	Gln	Thr	Leu	Thr	Pro	Ile	Leu	Gly	Ile	His	Gly
115							120				125				
Gly	Ser	Ser	Met	Ile	Met	Ala	Asp	Lys	Asp	Glu	Ser	Ser	Met	Phe	Phe
130							135				140				
Gln	Phe	Gly	Pro	Ser	Ile	Glu	Gln	Gln	Ala	Ser	Val	Met	Leu	Asn	Ile
145						150				155			160		
Met	Glu	Glu	Tyr	Asp	Trp	Tyr	Ile	Phe	Ser	Ile	Val	Thr	Thr	Tyr	Phe
165							170				175				
Pro	Gly	Tyr	Gln	Asp	Phe	Val	Asn	Lys	Ile	Arg	Ser	Thr	Ile	Glu	Asn
180							185				190				
Ser	Phe	Val	Gly	Trp	Glu	Leu	Glu	Glu	Val	Leu	Leu	Leu	Asp	Met	Ser
195						200				205					
Leu	Asp	Asp	Gly	Asp	Ser	Lys	Ile	Gln	Asn	Gln	Leu	Lys	Lys	Leu	Gln
210						215				220					
Ser	Pro	Ile	Ile	Leu	Leu	Tyr	Cys	Thr	Lys	Glu	Glu	Ala	Thr	Tyr	Ile
225						230				235			240		
Phe	Glu	Val	Ala	Asn	Ser	Val	Gly	Leu	Thr	Gly	Tyr	Gly	Tyr	Thr	Trp
245							250				255				
Ile	Val	Pro	Ser	Leu	Val	Ala	Gly	Asp	Thr	Asp	Thr	Val	Pro	Ala	Glu
260							265				270				
Phe	Pro	Thr	Gly	Leu	Ile	Ser	Val	Ser	Tyr	Asp	Glu	Trp	Asp	Tyr	Gly
275							280				285				
Leu	Pro	Pro	Arg	Val	Arg	Asp	Gly	Ile	Ala	Ile	Ile	Thr	Thr	Ala	Ala
290							295				300				
Ser	Asp	Met	Leu	Ser	Glu	His	Ser	Phe	Ile	Pro	Glu	Pro	Lys	Ser	Ser
305							310				315			320	
Cys	Tyr	Asn	Thr	His	Glu	Lys	Arg	Ile	Tyr	Gln	Ser	Asn	Met	Leu	Asn
325							330				335				
Arg	Tyr	Leu	Ile	Asn	Val	Thr	Phe	Glu	Gly	Arg	Asn	Leu	Ser	Phe	Ser
340							345				350				
Glu	Asp	Gly	Tyr	Gln	Met	His	Pro	Lys	Leu	Val	Ile	Ile	Leu	Leu	Asn
355							360				365				
Lys	Glu	Arg	Lys	Trp	Glu	Arg	Val	Gly	Lys	Trp	Lys	Asp	Lys	Ser	Leu

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375

380

Gln	Met	Lys	Tyr	Tyr	Val	Trp	Pro	Arg	Met	Cys	Pro	Glu	Thr	Glu	Glu
385					390				395			400			
Gln	Glu	Asp	Asp	His	Leu	Ser	Ile	Val	Thr	Leu	Glu	Glu	Ala	Pro	Phe
									410					415	
Val	Ile	Val	Glu	Ser	Val	Asp	Pro	Leu	Ser	Gly	Thr	Cys	Met	Arg	Asn
								425				430			
Thr	Val	Pro	Cys	Gln	Lys	Arg	Ile	Val	Thr	Glu	Asn	Lys	Thr	Asp	Glu
							435		440			445			
Glu	Pro	Gly	Tyr	Ile	Lys	Lys	Cys	Cys	Lys	Gly	Phe	Cys	Ile	Asp	Ile
					450				455			460			
Leu	Lys	Lys	Ile	Ser	Lys	Ser	Val	Lys	Phe	Thr	Tyr	Asp	Leu	Tyr	Leu
					465			470		475				480	
Val	Thr	Asn	Gly	Lys	His	Gly	Lys	Ile	Asn	Gly	Thr	Trp	Asn	Gly	
							485		490			495			
Met	Ile	Gly	Glu	Val	Val	Met	Lys	Arg	Ala	Tyr	Met	Ala	Val	Gly	Ser
						500			505			510			
Leu	Thr	Ile	Asn	Glu	Glu	Arg	Ser	Glu	Val	Val	Asp	Phe	Ser	Val	Pro
						515			520			525			
Phe	Ile	Glu	Thr	Gly	Ile	Ser	Val	Met	Val	Ser	Arg	Ser	Asn	Gly	Thr
						530			535			540			
Val	Ser	Pro	Ser	Ala	Phe	Leu	Glu	Pro	Phe	Ser	Ala	Asp	Val	Trp	Val
					545			550		555				560	
Met	Met	Phe	Val	Met	Leu	Leu	Ile	Val	Ser	Ala	Val	Ala	Val	Phe	Val
							565		570				575		
Phe	Glu	Tyr	Phe	Ser	Pro	Val	Gly	Tyr	Asn	Arg	Cys	Leu	Ala	Asp	Gly
						580			585			590			
Arg	Glu	Pro	Gly	Gly	Pro	Ser	Phe	Thr	Ile	Gly	Lys	Ala	Ile	Trp	Leu
							595		600			605			
Leu	Trp	Gly	Leu	Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Gln	Asn	Pro	Lys
						610			615			620			
Gly	Thr	Thr	Ser	Lys	Ile	Met	Val	Ser	Val	Trp	Ala	Phe	Phe	Ala	Val
						625			630		635			640	
Ile	Phe	Leu	Ala	Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln
						645			650			655			
Glu	Glu	Tyr	Val	Asp	Gln	Val	Ser	Gly	Leu	Ser	Asp	Lys	Lys	Phe	Gln
						660			665			670			
Arg	Pro	Asn	Asp	Phe	Ser	Pro	Pro	Phe	Arg	Phe	Gly	Thr	Val	Pro	Asn
						675			680			685			
Gly	Ser	Thr	Glu	Arg	Asn	Ile	Arg	Asn	Asn	Tyr	Ala	Glu	Met	His	Ala
						690			695			700			
Tyr	Met	Gly	Lys	Phe	Asn	Gln	Arg	Gly	Val	Asp	Asp	Ala	Leu	Leu	Ser
						705			710		715			720	
Leu	Lys	Thr	Gly	Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu
						725			730			735			

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Asn	Tyr	Met	Ala	Gly	Arg	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly
		740			745							750			
Ser	Gly	Lys	Val	Phe	Ala	Ser	Thr	Gly	Tyr	Gly	Ile	Ala	Ile	Gln	Lys
	755			760			765								
Asp	Ser	Gly	Trp	Lys	Arg	Gln	Val	Asp	Leu	Ala	Ile	Leu	Gln	Leu	Phe
	770			775			780								
Gly	Asp	Gly	Glu	Met	Glu	Glu	Leu	Glu	Ala	Leu	Trp	Leu	Thr	Gly	Ile
	785			790			795						800		
Cys	His	Asn	Glu	Lys	Asn	Glu	Val	Met	Ser	Ser	Gln	Leu	Asp	Ile	Asp
		805					810						815		
Asn	Met	Ala	Gly	Val	Phe	Tyr	Met	Leu	Gly	Ala	Ala	Met	Ala	Leu	Ser
		820					825					830			
Leu	Ile	Thr	Phe	Ile	Cys	Glu	His	Leu	Phe	Tyr	Trp	Gln	Phe	Arg	His
	835				840			845							
Cys	Phe	Met	Gly	Val	Cys	Ser	Gly	Lys	Pro	Gly	Met	Val	Phe	Ser	Ile
	850				855			860							
Ser	Arg	Gly	Ile	Tyr	Ser	Cys	Ile	His	Gly	Val	Ala	Ile	Glu	Glu	Arg
	865			870			875						880		
Gln	Ser	Val	Met	Asn	Ser	Pro	Thr	Ala	Thr	Met	Asn	Asn	Thr	His	Ser
		885					890					895			
Asn	Ile	Leu	Arg	Leu	Leu	Arg	Thr	Ala	Lys	Asn	Met	Ala	Asn	Leu	Ser
		900					905					910			
Gly	Val	Asn	Gly	Ser	Pro	Gln	Ser	Ala	Leu	Asp	Phe	Ile	Arg	Arg	Glu
	915					920					925				
Ser	Ser	Val	Tyr	Asp	Ile	Ser	Glu	His	Arg	Arg	Ser	Phe	Thr	His	Ser
	930				935			940							
Asp	Cys	Lys	Ser	Tyr	Asn	Asn	Pro	Pro	Cys	Glu	Glu	Asn	Leu	Phe	Ser
	945				950			955					960		
Asp	Tyr	Ile	Ser	Glu	Val	Glu	Arg	Thr	Phe	Gly	Asn	Leu	Gln	Leu	Lys
		965					970					975			
Asp	Ser	Asn	Val	Tyr	Gln	Asp	His	Tyr	His	His	His	Arg	Pro	His	
		980				985						990			
Ser	Ile	Gly	Ser	Ala	Ser	Ser	Ile	Asp	Gly	Leu	Tyr	Asp	Cys	Asp	Asn
		995					1000					1005			
Pro	Pro	Phe	Thr	Thr	Gln	Ser	Arg	Ser	Ile	Ser	Lys	Lys	Pro	Leu	Asp
	1010				1015			1020							
Ile	Gly	Leu	Pro	Ser	Ser	Lys	His	Ser	Gln	Leu	Ser	Asp	Leu	Tyr	Gly
	1025				1030			1035					1040		
Lys	Phe	Ser	Phe	Lys	Ser	Asp	Arg	Tyr	Ser	Gly	His	Asp	Asp	Leu	Ile
	1045					1050						1055			
Arg	Ser	Asp	Val	Ser	Asp	Ile	Ser	Thr	His	Thr	Val	Thr	Tyr	Gly	Asn
		1060				1065						1070			
Ile	Glu	Gly	Asn	Ala	Ala	Lys	Arg	Arg	Lys	Gln	Gln	Tyr	Lys	Asp	Ser
		1075				1080						1085			
Leu	Lys	Lys	Arg	Pro	Ala	Ser	Ala	Lys	Ser	Arg	Arg	Glu	Phe	Asp	Glu

1090	1095	1100
Ile Glu Leu Ala Tyr Arg Arg Arg Pro Pro Arg Ser Pro Asp His Lys 1105	1110	1115 1120
Arg Tyr Phe Arg Asp Lys Glu Gly Leu Arg Asp Phe Tyr Leu Asp Gln 1125	1130	1135
Phe Arg Thr Lys Glu Asn Ser Pro His Trp Glu His Val Asp Leu Thr 1140	1145	1150
Asp Ile Tyr Lys Glu Arg Ser Asp Asp Phe Lys Arg Asp Ser Ile Ser 1155	1160	1165
Gly Gly Gly Pro Cys Thr Asn Arg Ser His Ile Lys His Gly Thr Gly 1170	1175	1180
Asp Lys His Gly Val Val Ser Gly Val Pro Ala Pro Trp Glu Lys Asn 1185	1190	1195 1200
Leu Thr Asn Val Glu Trp Glu Asp Arg Ser Gly Gly Asn Phe Cys Arg 1205	1210	1215
Ser Cys Pro Ser Lys Leu His Asn Tyr Ser Thr Thr Val Thr Gly Gln 1220	1225	1230
Asn Ser Gly Arg Gln Ala Cys Ile Arg Cys Glu Ala Cys Lys Lys Ala 1235	1240	1245
Gly Asn Leu Tyr Asp Ile Ser Glu Asp Asn Ser Leu Gln Glu Leu Asp 1250	1255	1260
Gln Pro Ala Ala Pro Val Ala Val Thr Ser Asn Ala Ser Thr Thr Lys 1265	1270	1275 1280
Tyr Pro Gln Ser Pro Thr Asn Ser Lys Ala Gln Lys Lys Asn Arg Asn 1285	1290	1295
Lys Leu Arg Arg Gln His Ser Tyr Asp Thr Phe Val Asp Leu Gln Lys 1300	1305	1310
Glu Glu Ala Ala Leu Ala Pro Arg Ser Val Ser Leu Lys Asp Lys Gly 1315	1320	1325
Arg Phe Met Asp Gly Ser Pro Tyr Ala His Met Phe Glu Met Ser Ala 1330	1335	1340
Gly Glu Ser Thr Phe Ala Asn Asn Lys Ser Ser Val Pro Thr Ala Gly 1345	1350	1355 1360
His His His Asn Asn Pro Gly Gly Tyr Met Leu Ser Lys Ser 1365	1370	1375
Leu Tyr Pro Asp Arg Val Thr Gln Asn Pro Phe Ile Pro Thr Phe Gly 1380	1385	1390
Asp Asp Gln Cys Leu Leu His Gly Ser Lys Ser Tyr Phe Phe Arg Gln 1395	1400	1405
Pro Thr Val Ala Gly Ala Ser Lys Ala Arg Pro Asp Phe Arg Ala Leu 1410	1415	1420
Val Thr Asn Lys Pro Val Val Ser Ala Leu His Gly Ala Val Pro Ala 1425	1430	1435 1440
Arg Phe Gln Lys Asp Ile Cys Ile Gly Asn Gln Ser Asn Pro Cys Val 1445	1450	1455

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Pro Asn Asn Thr Asn Pro Arg Ala Phe Asn Gly Ser Ser Asn Gly His  
 1460 1465 1470

Val Tyr Glu Lys Leu Ser Ser Ile Glu Ser Asp Val  
 1475 1480

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4695 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 485..4495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CGAGAACACA GCGAGTGTGT GAGTCCTCC CGCTCCAGCT CCTCCAAGCC GCGGCCGCCG	60
CCGCCACCCCT CGCCCGCAGC CTCCCGCAGC CTCCCTCGGC CACCGGTGTC TGGTGGGGGT	120
GTTGCCTGGG TAGGTCGGCC CGGCCCGCAG GGGTCTCTCG AGCGTCTGCC ATCTGCCGA	180
GAAACATGTG TGGCACGTC CTCGCCTAGT CCAGGTGGCC GCAACCTTGG GGGAGAGACA	240
GGGCAGGACA GGACCAAGGT AAGAGGTAAG GAGGAGACGG CGCCAGGGAC AGACAGGAGG	300
TCCCAGGCTTG CCGTTGTGCG CACCACACT GCCGCCGCC CGGGGCCTGC CCCCCGACATC	360
GGCTCTCTGA GCCCTCCTCG GAATCTTGGG GTCGCTGGAC GCCGGGTTCC GGTCTGGCC	420
CCCCCGCCAT CCCCCCAACA GAACAGGGTC ATGAAAAGAG GCCGCCCGGC GGGGCCGCA	480
GGCG ATG CGC GGC GCC GGT GGC CCC CGC GGC CCT CGG GGC CCC GCT AAG Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys	529
1 5 10 15	
ATG CTG CTG CTG GCG CTG GCC TGC AGC CCG TTC CCG GAG GAG Met Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu	577
20 25 30	
GCG CCG GGG CCG GGC GGG GGT GGG CCC GGC GGC GGC CTC GGC GGG Ala Pro Gly Pro Gly Ala Gly Gly Pro Gly Gly Gly Leu Gly Gly	625
35 40 45	
GCG CGG CCG CTC AAC GTG GCG CTC GTG TTC TCG GGG CCC GCG TAC GCG Ala Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala	673
50 55 60	
GCC GAG GCG GCA CGC CTG GGC CCG GCC GTG GCG GCG GCG GTG CGC AGC Ala Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser	721
65 70 75	
CCG GGC CTA GAC GTG CGG CCC GTG GCG CTG GTG CTC AAC GGC TCG GAC Pro Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp	769
80 85 90 95	
CCG CGC AGC CTC GTG CTG CAG CTC TGC GAC CTG CTG TCG GGG TTG CGC Pro Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Ser Gly Leu Arg	817

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	100	105	110	
GTG CAC GGC GTG GTC TTC GAA GAC GAC TCG CGC GCG CCC GCC GTC GCG Val His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala	115	120	125	865
CCC ATC CTC GAC TTC CTG TCG GCG CAG ACC TCG CTC CCC ATC GTG TCC Pro Ile Leu Asp Phe Leu Ser Ala Gin Thr Ser Leu Pro Ile Val Ser	130	135	140	913
GAG CAC GGC GGC GCC GCG CTC GTG CTC ACG CCC AAG GAG AAG GGC TCC Glu His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser	145	150	155	961
ACC TTC CTC CAC CTG GGC TCT TCC CCC GAG CAA CAG CTT CAG GTC ATC Thr Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile	160	165	170	1009
TTT GAG GTG CTG GAG GAG TAT GAC TGG ACG TCC TTT GTA GCC GTG ACC Phe Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr	180	185	190	1057
ACT CGT GCC CCT GGC CAC CGG GCC TTC CTG TCC TAC ATT GAG GTG CTG Thr Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu	195	200	205	1105
ACT GAC GGC AGT CTG GTG GGC TGG GAG CAC CGC GGA GCG CTG ACG CTG Thr Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu	210	215	220	1153
GAC CCT GGG GCG GGC GAG GCC GTG CTC AGT GCC CAG CTC CGC AGT GTC Asp Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val	225	230	235	1201
AGC GCG CAG ATC CGC CTG CTC TTC TGC GCC CGA GAG GAG GCC GAG CCC Ser Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro	240	245	250	1249
GTG TTC CGC GCA GCT GAG GAG GCT GGC CTC ACT GGA TCT GGC TAC GTC Val Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val	260	265	270	1297
TGG TTC ATG GTG GGG CCC CAG CTG GCT GGA GGC GGG GGC TCT GGG GCC Trp Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Ser Gly Ala	275	280	285	1345
CCT GGT GAG CCC CCT CTT CTG CCA GGA GGC GCC CCC CTG CCT GCC GGG Pro Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly	290	295	300	1393
CTG TTT GCA GTG CGC TCG GCT GGC TGG CGG GAT GAC CTG GCT CGG CGA Leu Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg	305	310	315	1441
GTG GCA GCT GGG GTG GCC GTA GTG GGC AGA GGT GCC CAG GCC CTG CTG Val Ala Ala Gly Val Ala Val Ala Arg Gly Ala Gln Ala Leu Leu	320	325	330	1489
CGT GAT TAT GGT TTC CTT CCT GAG CTC GGC CAC GAC TGT CGC GCC CAG Arg Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln	340	345	350	1537
AAC CGC ACC CAC CGC GGG GAG AGT CTG CAT AGG TAC TTC ATG AAC ATC Asn Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile	355	360	365	1585
ACG TGG GAT AAC CGG GAT TAC TCC TTC AAT GAG GAC GGC TTC CTA GTG				1633

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Thr Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val		
370	375	380
AAC CCC TCC CTG GTG GTC ATC TCC CTC ACC AGA GAC AGG ACG TGG GAG		1681
Asn Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu		
385	390	395
GTG GTG GGC AGC TGG GAG CAG CAG ACG CTC CGC CTC AAG TAC CCG CTG		1729
Val Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu		
400	405	410
TGG TCC CGC TAT GGT CGC TTC CTG CAG CCA GTG GAC GAC ACG CAG CAC		1777
Trp Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His		
420	425	430
CTC GCG GTG GCC ACG CTG GAG GAA AGG CCG TTT GTC ATC GTG GAG CCT		1825
Leu Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro		
435	440	445
GCA GAC CCT ATC AGC GGC ACC TGC ATC CGA GAC TCC GTC CCC TGC CGG		1873
Ala Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg		
450	455	460
AGC CAG CTC AAC CGA ACC CAC AGC CCT CCA CCG GAT GCC CCC CGC CCG		1921
Ser Gln Leu Asn Arg Thr Ser Pro Pro Pro Asp Ala Pro Arg Pro		
465	470	475
GAA AAG CGC TGC TGC AAG GGT TTC TGC ATC GAC ATT CTG AAG CGG CTG		1969
Glu Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu		
480	485	490
GCG CAT ACC ATC GGC TTC AGC TAC GAC CTC TAC CTG GTC ACC AAT GGC		2017
Ala His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly		
500	505	510
AAG CAC GGA AAG AAG ATC GAT GGC GTC TGG AAC GGC ATG ATC GGG GAG		2065
Lys His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu		
515	520	525
GTG TTC TAC CAG CGC GCA GAC ATG GCC ATC GGC TCC CTC ACC ATC AAC		2113
Val Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn		
530	535	540
GAG GAG CGC TCC GAG ATC GTG GAC TTC TCC GTC CCC TTC GTG GAG ACC		2161
Glu Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr		
545	550	555
GGC ATC AGC GTC ATG GTG GCG CGC AGC AAT GGC ACG GTG TCC CCC TCG		2209
Gly Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser		
560	565	570
GCC TTC CTC GAG CCC TAC AGC CCC GCC GTG TGG GTG ATG ATG TTC GTC		2257
Ala Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val		
580	585	590
ATG TGC CTC ACT GTG GTC GCC GTC ACT GTT TTC ATC TTC GAG TAC CTC		2305
Met Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu		
595	600	605
AGT CCT GTT GGT TAC AAC CGC AGC CTG GCC ACG GGC AAG CGC CCT GGC		2353
Ser Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly		
610	615	620
GGT TCA ACC TTC ACC ATT GGG AAA TCC ATC TGG CTG CTC TGG GCC CTG		2401
Gly Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu		
625	630	635

GTG	TTC	AAT	AAT	TCG	GTG	CCC	GTG	GAG	AAC	CCC	CGG	GGA	ACC	ACC	AGC		2449
Val	Phe	Asn	Asn	Ser	Val	Pro	Val	Glu	Asn	Pro	Arg	Gly	Thr	Thr	Ser		
640					645					650					655		
AAA	ATC	ATG	GTG	CTG	GTG	TGG	GCC	TTC	TTC	GCC	GTC	ATC	TTC	CTC	GCC		2497
Lys	Ile	Met	Val	Leu	Val	Trp	Ala	Phe	Phe	Ala	Val	Ile	Phe	Leu	Ala		
					660				665					670			
AGC	TAC	ACA	GCC	AAC	CTG	GCC	GCC	TTC	ATG	ATC	CAG	GAG	GAG	TAC	GTG		2545
Ser	Tyr	Thr	Ala	Asn	Leu	Ala	Ala	Phe	Met	Ile	Gln	Glu	Glu	Tyr	Val		
					675				680					685			
GAT	ACT	GTG	TCT	GGG	CTC	AGT	GAC	CGC	AAG	TTC	CAG	AGG	CCC	CAG	GAG		2593
Asp	Thr	Val	Ser	Gly	Leu	Ser	Asp	Arg	Lys	Phe	Gln	Arg	Pro	Gln	Glu		
					690				695					700			
CAG	TAC	CCG	CCC	CTG	AAG	TTT	GGG	ACC	GTG	CCC	AAC	GGC	TCC	ACG	GAG		2641
Gln	Tyr	Pro	Pro	Leu	Lys	Phe	Gly	Thr	Val	Pro	Asn	Gly	Ser	Thr	Glu		
					705				710					715			
AAG	AAC	ATC	CGC	AGC	AAC	TAT	CCC	GAC	ATG	CAC	AGC	TAC	ATG	GTG	CGC		2689
Lys	Asn	Ile	Arg	Ser	Asn	Tyr	Pro	Asp	Met	His	Ser	Tyr	Met	Val	Arg		
					720				725					730			735
TAC	AAC	CAG	CCC	CGC	GTA	GAG	GAA	GCG	CTC	ACT	CAG	CTC	AAG	GCA	GGG		2737
Tyr	Asn	Gln	Pro	Arg	Val	Glu	Glu	Ala	Leu	Thr	Gln	Leu	Lys	Ala	Gly		
					740				745					750			
AAG	CTG	GAC	GCC	TTC	ATC	TAC	GAT	GCT	GCA	GTG	CTC	AAT	TAC	ATG	GCC		2785
Lys	Leu	Asp	Ala	Phe	Ile	Tyr	Asp	Ala	Ala	Val	Leu	Asn	Tyr	Met	Ala		
					755				760					765			
CGC	AAG	GAC	GAG	GGC	TGC	AAG	CTT	GTC	ACC	ATC	GGC	TCC	GGC	AAG	GTC		2833
Arg	Lys	Asp	Glu	Gly	Cys	Lys	Leu	Val	Thr	Ile	Gly	Ser	Gly	Lys	Val		
					770				775					780			
TTC	GCC	ACG	ACA	GGC	TAT	GGC	ATC	GCC	CTG	CAC	AAG	GGC	TCC	CGC	TGG		2881
Phe	Ala	Thr	Thr	Gly	Tyr	Gly	Ile	Ala	Leu	His	Lys	Gly	Ser	Arg	Trp		
					785				790					795			
AAG	CGG	CCC	ATC	GAC	CTG	GCG	TTG	CTG	CAG	TTC	CTG	GGG	GAT	GAT	GAG		2929
Lys	Arg	Pro	Ile	Asp	Leu	Ala	Leu	Leu	Gln	Phe	Leu	Gly	Asp	Asp	Glu		
					800				805					810			815
ATC	GAG	ATG	CTG	GAG	CGG	CTG	TGG	CTC	TCT	GGG	ATC	TGC	CAC	AAT	GAC		2977
Ile	Glu	Met	Leu	Glu	Arg	Leu	Trp	Leu	Ser	Gly	Ile	Cys	His	Asn	Asp		
					820				825					830			
AAA	ATC	GAG	GTG	ATG	AGC	AAG	CTG	GAC	ATC	GAC	AAC	ATG	GCG	GGC			3025
Lys	Ile	Glu	Val	Met	Ser	Ser	Lys	Leu	Asp	Ile	Asp	Asn	Met	Ala	Gly		
					835				840					845			
GTC	TTC	TAC	ATG	CTC	CTG	GTG	GCC	ATG	GGC	CTG	TCC	CTG	CTG	GTC	TTC		3073
Val	Phe	Tyr	Met	Leu	Leu	Val	Ala	Met	Gly	Leu	Ser	Leu	Leu	Val	Phe		
					850				855					860			
GCC	TGG	GAG	CAC	CTG	GTG	TAC	TGG	CGC	CTG	CGG	CAC	TGC	CTG	GGG	CCC		3121
Ala	Trp	Glu	His	Leu	Val	Tyr	Trp	Arg	Leu	Arg	His	Cys	Leu	Gly	Pro		
					865				870					875			
ACC	CAC	CGC	ATG	GAC	TTC	CTG	CTG	GCC	TTC	TCC	AGG	GGC	ATG	TAC	AGC		3169
Thr	His	Arg	Met	Asp	Phe	Leu	Leu	Ala	Phe	Ser	Arg	Gly	Met	Tyr	Ser		
					880				885					890			895
TGC	TGC	AGC	GCT	GAG	GCC	GCC	CCA	CCG	CCC	GCC	AAG	CCC	CCG	CCG	CCG		3217
Cys	Cys	Ser	Ala	Glu	Ala	Ala	Pro	Pro	Pro	Pro	Ala	Lys	Pro	Pro	Pro		
					900				905					910			

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CCA CAG CCC CTG CCC AGC CCC GCG TAC CCC GCG CCG GGG CCG GCT CCC		3265
Pro Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro		
915 920 925		
GGG CCC GCA CCT TTC GTC CCC CGC GAG CGC GCC TCA GTG GCC CGC TGG		3313
Gly Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp		
930 935 940		
CGC CGG CCC AAG GGC GCG GGG CCG CCG GGG GGC GCG GGC CTG GCC GAC		3361
Arg Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp		
945 950 955		
GGC TTC CAC CGC TAC TAC GGC CCC ATC GAG CCG CAG GGC CTA GGC CTC		3409
Gly Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu		
960 965 975		
GGC CTG GGC GAA GCG CGC GCG GCA CCG CGG GGC GCA GCC GGG CGC CCG		3457
Gly Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro		
980 985 990		
CTG TCC CCG CCG GCC GCT CAG CCC CCG CAG AAG CCG CCG GCC TCC TAT		3505
Leu Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr		
995 1000 1005		
TTC GCC ATC GTA CGC GAC AAG GAG CCA GCC GAG CCC CCC GCC GGC GGC		3553
Phe Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala		
1010 1015 1020		
TTC CCC GGC TTC CCG TCC CCG CCC GCG CCC CCC GCC GCC GCG GCC ACC		3601
Phe Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr		
1025 1030 1035		
GCC GTC GGG CCG CCA CTC TGC CGC TTG GCC TTC GAG GAC GAG AGC CCG		3649
Ala Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro		
1040 1045 1050 1055		
CCG GCG CCC GCG CGG TGG CCG CGC TCG GAC CCC GAG AGC CAA CCC CTG		3697
Pro Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu		
1060 1065 1070		
CTG GGG CCA GGC GCG GGC GCG GGG GGC ACG GGG GGC GCA GGC GGA		3745
Leu Gly Pro Gly Ala Gly Gly Ala Gly Thr Gly Gly Ala Gly Gly		
1075 1080 1085		
GGA GCC CCG GCC GCT CCG CCC CCG TGC TTC GCC GCG CCG CCC CCG TGC		3793
Gly Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys		
1090 1095 1100		
TTT TAC CTC GAT GTC GAC CAG TCG CCG TCG GAC TCG GAG GAC TCG GAG		3841
Phe Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu		
1105 1110 1115		
AGC CTG GCC GGC GCG TCC CTG GCC GGC CTG GAT CCC TGG TGG TTC GCC		3889
Ser Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala		
1120 1125 1130 1135		
GAC TTC CCT TAC CCG TAT GCC GAT CGC CTC GGG CSG CCC GCG GCA CGC		3937
Asp Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg		
1140 1145 1150		
TAC GGA TTG GTC GAC AAA CTA GGG GGC TGG CTC GCC GGG AGC TGG GAC		3985
Tyr Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp		
1155 1160 1165		
TAC CTG CCT CCS CGC AGC GGT CGG GCC TGG CAC TGT CGG CAC TGC		4033
Tyr Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys		
1170 1175 1180		

GCC AGC CTG GAG CTG CTT CCG CCG CCG CGC CAT CTC AGC TGC TCG CAC Ala Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His 1185 1190 1195	4081
GAT GGC CTG GAC GGC GGC TGG TGG GCG CCA CCT CCA CCC TGG GCC Asp Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Pro Trp Ala 1200 1205 1210 1215	4129
GCC GGG CCC CTG CCC CGA CGC CGG GCC CGC TGC GGG TGC CCG CGG TCG Ala Gly Pro Leu Pro Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser 1220 1225 1230	4177
CAC CCG CAC CGC CCG CGG GCC TCG CAC CGC ACG CCC GCC GCT GCC GCG His Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala 1235 1240 1245	4225
CCC CAC CAC CAC AGG CAC CGG CGC GCC GCT GGG GGC TGG GAC CTC CCG Pro His His His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro 1250 1255 1260	4273
CCG CCC GCG CCC ACC TCG CGC TCG CTC GAG GAC CTC AGC TCG TGC CCT Pro Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro 1265 1270 1275	4321
CGC GCC GCC CCT GCG CGC AGG CTT ACC GGG CCC TCC CGC CAC GCT CGC Arg Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg 1280 1285 1290 1295	4369
AGG TGT CCG CAC GCC GCG CAC TGG GGG CCG CCTG CCT ACA GCT TCC Arg Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser 1300 1305 1310	4417
CAC CGG AGA CAC CGG GGG GAC CCTG GGC ACC CGC AGG GGC TCG GCG His Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala 1315 1320 1325	4465
CAC TTC TCT AGC CTC GAG TCC GAG GTA TGACGCCGGCC CGGGGGGCC His Phe Ser Ser Leu Glu Ser Glu Val 1330 1335	4512
CACCGCCCCC TTGGTCAGCG CAGGCCACGG CCCGAGGGGG CGCCCGCAGT GGACAGGACC	4572
CGCGTGGGTT GGGAAAGGAAA GCAGTGGAAC TGGCCGGACC CGGCCTGGAG CAGCGTCCTG	4632
CGCCCCCTGG TTCTGGAGGA ACCGCAAGCC GGAGAGGATT TGGTCCCTCA ACTATCACCC	4692
AGG	4695

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 1336 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Met Arg Gly Ala Gly Gly Pro Arg Gly Pro Arg Gly Pro Ala Lys Met  
1 5 10 15

Leu Leu Leu Leu Ala Leu Ala Cys Ala Ser Pro Phe Pro Glu Glu Ala  
20 25 30

Pro Gly Pro Gly Gly Ala Gly Gly Pro Gly Gly Leu Gly Gly Ala

35	40	45
Arg Pro Leu Asn Val Ala Leu Val Phe Ser Gly Pro Ala Tyr Ala Ala		
50	55	60
Glu Ala Ala Arg Leu Gly Pro Ala Val Ala Ala Val Arg Ser Pro		
65	70	75
80		
Gly Leu Asp Val Arg Pro Val Ala Leu Val Leu Asn Gly Ser Asp Pro		
85	90	95
Arg Ser Leu Val Leu Gln Leu Cys Asp Leu Leu Ser Gly Leu Arg Val		
100	105	110
His Gly Val Val Phe Glu Asp Asp Ser Arg Ala Pro Ala Val Ala Pro		
115	120	125
Ile Leu Asp Phe Leu Ser Ala Gln Thr Ser Leu Pro Ile Val Ser Glu		
130	135	140
His Gly Gly Ala Ala Leu Val Leu Thr Pro Lys Glu Lys Gly Ser Thr		
145	150	155
160		
Phe Leu His Leu Gly Ser Ser Pro Glu Gln Gln Leu Gln Val Ile Phe		
165	170	175
Glu Val Leu Glu Glu Tyr Asp Trp Thr Ser Phe Val Ala Val Thr Thr		
180	185	190
Arg Ala Pro Gly His Arg Ala Phe Leu Ser Tyr Ile Glu Val Leu Thr		
195	200	205
Asp Gly Ser Leu Val Gly Trp Glu His Arg Gly Ala Leu Thr Leu Asp		
210	215	220
Pro Gly Ala Gly Glu Ala Val Leu Ser Ala Gln Leu Arg Ser Val Ser		
225	230	235
240		
Ala Gln Ile Arg Leu Leu Phe Cys Ala Arg Glu Glu Ala Glu Pro Val		
245	250	255
Phe Arg Ala Ala Glu Glu Ala Gly Leu Thr Gly Ser Gly Tyr Val Trp		
260	265	270
Phe Met Val Gly Pro Gln Leu Ala Gly Gly Gly Ser Gly Ala Pro		
275	280	285
Gly Glu Pro Pro Leu Leu Pro Gly Gly Ala Pro Leu Pro Ala Gly Leu		
290	295	300
Phe Ala Val Arg Ser Ala Gly Trp Arg Asp Asp Leu Ala Arg Arg Val		
305	310	315
320		
Ala Ala Gly Val Ala Val Val Ala Arg Gly Ala Gln Ala Leu Leu Arg		
325	330	335
Asp Tyr Gly Phe Leu Pro Glu Leu Gly His Asp Cys Arg Ala Gln Asn		
340	345	350
Arg Thr His Arg Gly Glu Ser Leu His Arg Tyr Phe Met Asn Ile Thr		
355	360	365
Trp Asp Asn Arg Asp Tyr Ser Phe Asn Glu Asp Gly Phe Leu Val Asn		
370	375	380
Pro Ser Leu Val Val Ile Ser Leu Thr Arg Asp Arg Thr Trp Glu Val		
385	390	395
400		

Val Gly Ser Trp Glu Gln Gln Thr Leu Arg Leu Lys Tyr Pro Leu Trp  
405 410 415

Ser Arg Tyr Gly Arg Phe Leu Gln Pro Val Asp Asp Thr Gln His Leu  
420 425 430

Ala Val Ala Thr Leu Glu Glu Arg Pro Phe Val Ile Val Glu Pro Ala  
435 440 445

Asp Pro Ile Ser Gly Thr Cys Ile Arg Asp Ser Val Pro Cys Arg Ser  
450 455 460

Gln Leu Asn Arg Thr His Ser Pro Pro Pro Asp Ala Pro Arg Pro Glu  
465 470 475 480

Lys Arg Cys Cys Lys Gly Phe Cys Ile Asp Ile Leu Lys Arg Leu Ala  
485 490 495

His Thr Ile Gly Phe Ser Tyr Asp Leu Tyr Leu Val Thr Asn Gly Lys  
500 505 510

His Gly Lys Lys Ile Asp Gly Val Trp Asn Gly Met Ile Gly Glu Val  
515 520 525

Phe Tyr Gln Arg Ala Asp Met Ala Ile Gly Ser Leu Thr Ile Asn Glu  
530 535 540

Glu Arg Ser Glu Ile Val Asp Phe Ser Val Pro Phe Val Glu Thr Gly  
545 550 555 560

Ile Ser Val Met Val Ala Arg Ser Asn Gly Thr Val Ser Pro Ser Ala  
565 570 575

Phe Leu Glu Pro Tyr Ser Pro Ala Val Trp Val Met Met Phe Val Met  
580 585 590

Cys Leu Thr Val Val Ala Val Thr Val Phe Ile Phe Glu Tyr Leu Ser  
595 600 605

Pro Val Gly Tyr Asn Arg Ser Leu Ala Thr Gly Lys Arg Pro Gly Gly  
610 615 620

Ser Thr Phe Thr Ile Gly Lys Ser Ile Trp Leu Leu Trp Ala Leu Val  
625 630 635 640

Phe Asn Asn Ser Val Pro Val Glu Asn Pro Arg Gly Thr Thr Ser Lys  
645 650 655

Ile Met Val Leu Val Trp Ala Phe Phe Ala Val Ile Phe Leu Ala Ser  
660 665 670

Tyr Thr Ala Asn Leu Ala Ala Phe Met Ile Gln Glu Glu Tyr Val Asp  
675 680 685

Thr Val Ser Gly Leu Ser Asp Arg Lys Phe Gln Arg Pro Gln Glu Gln  
690 695 700

Tyr Pro Pro Leu Lys Phe Gly Thr Val Pro Asn Gly Ser Thr Glu Lys  
705 710 715 720

Asn Ile Arg Ser Asn Tyr Pro Asp Met His Ser Tyr Met Val Arg Tyr  
725 730 735

Asn Gln Pro Arg Val Glu Glu Ala Leu Thr Gln Leu Lys Ala Gly Lys  
740 745 750

Leu Asp Ala Phe Ile Tyr Asp Ala Ala Val Leu Asn Tyr Met Ala Arg

755	760	765
Lys Asp Glu Gly Cys Lys Leu Val Thr Ile Gly Ser Gly Lys Val Phe		
770	775	780
Ala Thr Thr Gly Tyr Gly Ile Ala Leu His Lys Gly Ser Arg Trp Lys		
785	790	795
800		
Arg Pro Ile Asp Leu Ala Leu Gln Phe Leu Gly Asp Asp Glu Ile		
805	810	815
Glu Met Leu Glu Arg Leu Trp Leu Ser Gly Ile Cys His Asn Asp Lys		
820	825	830
Ile Glu Val Met Ser Ser Lys Leu Asp Ile Asp Asn Met Ala Gly Val		
835	840	845
Phe Tyr Met Leu Leu Val Ala Met Gly Leu Ser Leu Leu Val Phe Ala		
850	855	860
Trp Glu His Leu Val Tyr Trp Arg Leu Arg His Cys Leu Gly Pro Thr		
865	870	875
880		
His Arg Met Asp Phe Leu Leu Ala Phe Ser Arg Gly Met Tyr Ser Cys		
885	890	895
Cys Ser Ala Glu Ala Ala Pro Pro Pro Ala Lys Pro Pro Pro Pro Pro		
900	905	910
Gln Pro Leu Pro Ser Pro Ala Tyr Pro Ala Pro Gly Pro Ala Pro Gly		
915	920	925
Pro Ala Pro Phe Val Pro Arg Glu Arg Ala Ser Val Ala Arg Trp Arg		
930	935	940
Arg Pro Lys Gly Ala Gly Pro Pro Gly Gly Ala Gly Leu Ala Asp Gly		
945	950	955
960		
Phe His Arg Tyr Tyr Gly Pro Ile Glu Pro Gln Gly Leu Gly Leu Gly		
965	970	975
Leu Gly Glu Ala Arg Ala Ala Pro Arg Gly Ala Ala Gly Arg Pro Leu		
980	985	990
Ser Pro Pro Ala Ala Gln Pro Pro Gln Lys Pro Pro Ala Ser Tyr Phe		
995	1000	1005
Ala Ile Val Arg Asp Lys Glu Pro Ala Glu Pro Pro Ala Gly Ala Phe		
1010	1015	1020
Pro Gly Phe Pro Ser Pro Pro Ala Pro Pro Ala Ala Ala Ala Thr Ala		
1025	1030	1035
1040		
Val Gly Pro Pro Leu Cys Arg Leu Ala Phe Glu Asp Glu Ser Pro Pro		
1045	1050	1055
Ala Pro Ala Arg Trp Pro Arg Ser Asp Pro Glu Ser Gln Pro Leu Leu		
1060	1065	1070
Gly Pro Gly Ala Gly Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Gly		
1075	1080	1085
Ala Pro Ala Ala Pro Pro Pro Cys Phe Ala Ala Pro Pro Pro Cys Phe		
1090	1095	1100
Tyr Leu Asp Val Asp Gln Ser Pro Ser Asp Ser Glu Asp Ser Glu Ser		
1105	1110	1115
1120		

Leu Ala Gly Ala Ser Leu Ala Gly Leu Asp Pro Trp Trp Phe Ala Asp  
1125 1130 1135

Phe Pro Tyr Pro Tyr Ala Asp Arg Leu Gly Xaa Pro Ala Ala Arg Tyr  
1140 1145 1150

Gly Leu Val Asp Lys Leu Gly Gly Trp Leu Ala Gly Ser Trp Asp Tyr  
1155 1160 1165

Leu Pro Xaa Arg Ser Gly Arg Ala Ala Trp His Cys Arg His Cys Ala  
1170 1175 1180

Ser Leu Glu Leu Leu Pro Pro Pro Arg His Leu Ser Cys Ser His Asp  
1185 1190 1195 1200

Gly Leu Asp Gly Gly Trp Trp Ala Pro Pro Pro Pro Trp Ala Ala  
1205 1210 1215

Gly Pro Leu Pro Arg Arg Ala Arg Cys Gly Cys Pro Arg Ser His  
1220 1225 1230

Pro His Arg Pro Arg Ala Ser His Arg Thr Pro Ala Ala Ala Pro  
1235 1240 1245

His His His Arg His Arg Arg Ala Ala Gly Gly Trp Asp Leu Pro Pro  
1250 1255 1260

Pro Ala Pro Thr Ser Arg Ser Leu Glu Asp Leu Ser Ser Cys Pro Arg  
1265 1270 1275 1280

Ala Ala Pro Ala Arg Arg Leu Thr Gly Pro Ser Arg His Ala Arg Arg  
1285 1290 1295

Cys Pro His Ala Ala His Trp Gly Pro Pro Leu Pro Thr Ala Ser His  
1300 1305 1310

Arg Arg His Arg Gly Gly Asp Leu Gly Thr Arg Arg Gly Ser Ala His  
1315 1320 1325

Phe Ser Ser Leu Glu Ser Glu Val  
1330 1335

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: both  
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GGGTGGCGGC CGCAGAGCAC CTCCACCATC TCCTTGTCT ACTCCAAGAT CTGGCCCTAG 60  
TCCATGTTTG C 71

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TGGTGGTCCC CAACCTGTAG GACTGGTTC TGGAGGAGGA TCTGGTAG GC AACATGG	60
ACTAGGGCCA G	71

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 61 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTTGGGGACC ACCAGATGGA GGTAGAGCTG CACTTGTACG AAGAGCTCCA CAACCACCTG	60
G	61

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 62 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGTGAGACGT CAGACAAAGG AGGCCAGGT GTAGGTGGTC TACCAAGTGG TTGTGGAGCT	60
CT	62

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 195 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: both
  - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CCGCAGAGCA CCTCCACCAT CTCCCTGTCC TACTCCAAGA TCTGGCCCTA GTCCATGTTT	60
GCCTACACCA GATCCTCCTC CAGAACCAAG TCCTACAGGT TGGGGACAC CAGATGGAGG	120
TAGAGCTGCA CTTGTACGAA GAGCTCCACA ACCACCTGGT AGACCACCTA CACCTGGGCC	180
TCCTTGTCT GACGT	195

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*Scanned copy is best available sequence listing on page  
68 to 164 in specification*